

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Wild, Martha A.
Cochran, Mark D.
- (ii) TITLE OF INVENTION: RECOMBINANT INFECTIOUS LARYNGOTRACHEITIS VIRUS
AND USES THEREOF
- (iii) NUMBER OF SEQUENCES: 72
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Cooper & Dunham LLP
 - (B) STREET: 1185 Avenue of the Americas
 - (C) CITY: New York
 - (D) STATE: New York
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 10036
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE: 23-MAR-1995
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/126,597
 - (B) FILING DATE: 24-SEP-1993
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: White, John P.
 - (B) REGISTRATION NUMBER: 28,678
 - (C) REFERENCE/DOCKET NUMBER: 39116-A
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (212) 278-0400
 - (B) TELEFAX: (212) 391-0525

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13473 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1059..2489
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2575..4107

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 4113..4445

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 4609..5487

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 5697..8654

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 9874..10962

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 11159..12658

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 12665..13447

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCCGTGCCCC TAAAGGCCGC CGAGAAAGCT AAGTCCAAAT GTGACGTCGG AGGTCTCGAC	60
ATGGTCGCCA ACCCTCCAAA TGCTACCCGC CGGCCACGC AACCGGGCT TTTATAAAGA	120
TGGCGCGCGA GACAATAACA CTTACTCATC CGCGTACGCG TTTATTATTG TCAATATTTG	180
TGTGGTTATT ATTACTGCTA CCGCCCTTGT TTCTGCAAGG CCCTCGCCGC GGCCCAGGCC	240
ACTATTCCGG CAGCGGCCGC CGACGCGGCG AGCGTCGCCG CTAACGTCGG CGCCGCGGGG	300
AGCGGGGTTT CTTGCGACTTA AATAGACTCC CGAGAAAAAA TTTTGGCTGC CGTTCGCCAT	360
CATCCGAGTC GGAAACACAG TATGCGGCCG AGTTAGGTTT TACTTTTAAA AACTTTACCG	420
TGCTGTACGG CCAGGGCGTT CTCAGGCTCG AAGGGGCAAG AGTTGTCCAG ACTGATGGGT	480
GACTCAGAGA CAGCGTTGTC TTGTCTCCGT TTACCAAAAA TATTTCCACT CCTCTCTCAA	540
AATTTTTTACC TCCGGTTTCG GTAATTAGGA AAGTTTTTGG CGCAGGGAGG TTTAAAGCTG	600
CCATGCATAT GTCAGCGGTA CCCAGCACCC ACAAATGGAA CTCTTTTGCG GCATACGCGC	660
CAGATGACAA ATGGTAAAAC CCTGCGTCCA AGCCGCTCCA CTCGGGACTT ACTCCAGGCG	720
GGTCGCCCCC CTCACCGAAC CGAATCACGG GTCTGCACAT CCTGGGAAGG GAAAACAGCT	780
CCCCGGAAC TTCGTACAGA GATGCCGGGC GCACGATTAC CGATAATGTA CTCGGACGAT	840
CGTAACTCGC CATAGTTTTC ACTGCGTGAA CCAATTCTTT CCATCCAGAA TCCGAGAGCT	900
CAAATCTAGA ATTAGGTAGT TTGTAGTGCG AATCGACCGC AGAAACTATA GTCACTTTTA	960
CAGGCGCCAT CGCCGCTCAG ACTCCACCCC GCTATGATGT CAGAAATATA ACGCTCTTAT	1020
TCTAGCAGAG TCAGGCCAAT ATATACAGCT TAGAGAAG ATG CGG TTT CGG CGC	1073
Met Arg Phe Arg Arg	
1 5	
ATC TGT TCA CGC TCT AGG GCA GAA AAA CGA AGA AGA ACA ACC GAG AAT	1121
Ile Cys Ser Arg Ser Arg Ala Glu Lys Arg Arg Arg Thr Thr Glu Asn	
10 15 20	

GAC ACC TCG CGC TTC GAG CCT GCG CTG GGC TGT TTG TCA GAG TAC TTT Asp Thr Ser Arg Phe Glu Pro Ala Leu Gly Cys Leu Ser Glu Tyr Phe 340 345 350	3630
GCA CTA GTG GTG TTA CTG GCC GAG ACG GTC TTA GCG ACC ATG TTC GAC Ala Leu Val Val Leu Leu Ala Glu Thr Val Leu Ala Thr Met Phe Asp 355 360 365	3678
CAC GCA CTG GTA TTC ATG AGG GCG CTG GCA GAC GGC AAT TTC GAT GAC His Ala Leu Val Phe Met Arg Ala Leu Ala Asp Gly Asn Phe Asp Asp 370 375 380	3726
TAT GAC GAA ACT AGA TAT ATA GAC CCC GTT AAA AAC GAG TAC CTG AAC Tyr Asp Glu Thr Arg Tyr Ile Asp Pro Val Lys Asn Glu Tyr Leu Asn 385 390 395 400	3774
GGA GCC GAG GGT ACT CTG TTA CGG GGC ATA GTG GCC TCC AAC ACC GCT Gly Ala Glu Gly Thr Leu Leu Arg Gly Ile Val Ala Ser Asn Thr Ala 405 410 415	3822
CTG GCG GTG GTT TGC GCA AAC ACC TAT TCG ACG ATA AGA AAA CTC CCG Leu Ala Val Val Cys Ala Asn Thr Tyr Ser Thr Ile Arg Lys Leu Pro 420 425 430	3870
TCC GTG GCA ACT AGC GCG TGC AAT GTT GCC TAC AGG ACC GAA ACG CTG Ser Val Ala Thr Ser Ala Cys Asn Val Ala Tyr Arg Thr Glu Thr Leu 435 440 445	3918
AAA GCG AGG CGC CCT GGC ATG AGC GAC ATA TAC CGG ATA TTA CAA AAA Lys Ala Arg Arg Pro Gly Met Ser Asp Ile Tyr Arg Ile Leu Gln Lys 450 455 460	3966
GAG TTT TTC TTT TAC ATT GCG TGG CTC CAG AGG GTT GCA ACA CAC GCA Glu Phe Phe Phe Tyr Ile Ala Trp Leu Gln Arg Val Ala Thr His Ala 465 470 475 480	4014
AAT TTC TGT TTA AAC ATT CTG AAG AGA AGC GTG GAT ACG GGC CCC CGC Asn Phe Cys Leu Asn Ile Leu Lys Arg Ser Val Asp Thr Gly Pro Arg 485 490 495	4062
CAT TTT TGT TCA GGG CCA GCT CGG AGA AGC GGC TGC AGC AGT TAAATAAA His Phe Cys Ser Gly Pro Ala Arg Arg Ser Gly Cys Ser 500 505 510	4112
ATG CTC TGC CCC CTT CTC GTG CCG ATT CAA TAT GAA GAC TTT TCG AAG Met Leu Cys Pro Leu Leu Val Pro Ile Gln Tyr Glu Asp Phe Ser Lys 1 5 10 15	4160
GCC ATG GGG TCT GAG CTC AAG AGG GAA AAG TTA GAG ACA TTC GTT AAA Ala Met Gly Ser Glu Leu Lys Arg Glu Lys Leu Glu Thr Phe Val Lys 20 25 30	4208
GCT ATT TCC AGC GAC AGG GAC CCG AGG GGG TCC TTA AGA TTT CTC ATT Ala Ile Ser Ser Asp Arg Asp Pro Arg Gly Ser Leu Arg Phe Leu Ile 35 40 45	4256
TCG GAC CAT GCA AGG GAA ATT ATT GCA GAC GGA GTA CGG TTT AAG CCG Ser Asp His Ala Arg Glu Ile Ile Ala Asp Gly Val Arg Phe Lys Pro 50 55 60	4304
GTG ATA GAC GAG CCG GTT CGG GCT TCA GTT GCG CTG AGT ACC GCT GCC Val Ile Asp Glu Pro Val Arg Ala Ser Val Ala Leu Ser Thr Ala Ala 65 70 75 80	4352
GCT GGG AAA GTG AAA GCG CGA CGC TTA ACC TCA GTT CGC GCG CCC GTA Ala Gly Lys Val Lys Ala Arg Arg Leu Thr Ser Val Arg Ala Pro Val 85 90 95	4400

CCG CCC GCA GGC GCC GTT TCC GCG CGC CGG AAA TCG GAA ATA TGA TA 4447
Pro Pro Ala Gly Ala Val Ser Ala Arg Arg Lys Ser Glu Ile *
100 105 110

AAAAATGCTTG GCATTTGCGG GCGAAGAGGC GTGATCTGAA GGGCTCCACA ATGACGTAAC 4507

TGAGCTACGC ATCCCTATAA AGTGACSCG CTGACCGCTA GCCCATAACAG TGTTACAGGA 4567

GGGGAGAGAG ACAACTTCAG CTCGAAGTCT GAAGAGACAT C ATG AGC GGC 4617
Met Ser Gly
1

TTC AGT AAC ATA GGA TCG ATT GCC ACC GTT TCC CTA GTA TGC TCG CTT 4665
Phe Ser Asn Ile Gly Ser Ile Ala Thr Val Ser Leu Val Cys Ser Leu
5 10 15

TTG TGC GCA TCT GTA TTA GGG GCG CCG GTA CTG GAC GGG CTC GAG TCG 4713
Leu Cys Ala Ser Val Leu Gly Ala Pro Val Leu Asp Gly Leu Glu Ser
20 25 30 35

AGC CCT TTC CCG TTC GGG GGC AAA ATT ATA GCC CAG GCG TGC AAC CGC 4761
Ser Pro Phe Pro Phe Gly Gly Lys Ile Ile Ala Gln Ala Cys Asn Arg
40 45 50

ACC ACG ATT GAG GTG ACG GTC CCG TGG AGC GAC TAC TCT GGT CGC ACC 4809
Thr Thr Ile Glu Val Thr Val Pro Trp Ser Asp Tyr Ser Gly Arg Thr
55 60 65

GAA GGA GTG TCA GTC GAG GTG AAA TGG TTC TAC GGG AAT AGT AAT CCC 4857
Glu Gly Val Ser Val Glu Val Lys Trp Phe Tyr Gly Asn Ser Asn Pro
70 75 80

GAA AGC TTC GTG TTC GGG GTG GAT AGC GAA ACG GGC AGT GGA CAC GAG 4905
Glu Ser Phe Val Phe Gly Val Asp Ser Glu Thr Gly Ser Gly His Glu
85 90 95

GAC CTG TCT ACG TGC TGG GCT CTA ATC CAT AAT CTG AAC GCG TCT GTG 4953
Asp Leu Ser Thr Cys Trp Ala Leu Ile His Asn Leu Asn Ala Ser Val
100 105 110 115

TGC AGG GCG TCT GAC GCC GGG ATA CCT GAT TTC GAC AAG CAG TGC GAA 5001
Cys Arg Ala Ser Asp Ala Gly Ile Pro Asp Phe Asp Lys Gln Cys Glu
120 125 130

AAA GTG CAG AGA AGA CTG CGC TCC GGG GTG GAA CTT GGT AGT TAC GTG 5049
Lys Val Gln Arg Arg Leu Arg Ser Gly Val Glu Leu Gly Ser Tyr Val
135 140 145

TCT GGC AAT GGA TCC CTG GTG CTG TAC CCA GGG ATG TAC GAT GCC GGC 5097
Ser Gly Asn Gly Ser Leu Val Leu Tyr Pro Gly Met Tyr Asp Ala Gly
150 155 160

ATC TAC GCC TAC CAG CTC TCA GTG GGT GGG AAG GGA TAT ACC GGG TCT 5145
Ile Tyr Ala Tyr Gln Leu Ser Val Gly Gly Lys Gly Tyr Thr Gly Ser
165 170 175

GTT TAT CTA GAC GTC GGA CCA AAC CCC GGA TGC CAC GAC CAG TAT GGG 5193
Val Tyr Leu Asp Val Gly Pro Asn Pro Gly Cys His Asp Gln Tyr Gly
180 185 190 195

TAC ACC TAT TAC AGC CTG GCC GAC GAG GCG TCA GAC TTA TCA TCT TAT 5241
Tyr Thr Tyr Tyr Ser Leu Ala Asp Glu Ala Ser Asp Leu Ser Ser Tyr
200 205 210

GAC GTA GCC TCG CCC GAA CTC GAC GGT CCT ATG GAG GAA GAT TAT TCC 5289
Asp Val Ala Ser Pro Glu Leu Asp Gly Pro Met Glu Glu Asp Tyr Ser
215 220 225

CGT	CGT	TGG	TTA	GGC	CCC	CCG	TCG	CCT	TAT	GTG	CGA	GAT	AAC	GAT	GTC	6236
Lys	Arg	Trp	Leu	Gly	Pro	Pro	Ser	Pro	Tyr	Val	Arg	Asp	Asn	Asp	Val	
165				170						175					180	
GCC	GTG	TTG	ACA	AAA	GCG	CAG	TAC	ATT	GGG	GAG	TGC	TAC	TCC	AAC	TCG	6284
Ala	Val	Leu	Thr	Lys	Ala	Gln	Tyr	Ile	Gly	Glu	Cys	Tyr	Ser	Asn	Ser	
				185					190						195	
GCG	GCC	CAG	ACG	GGG	CTC	ACG	TCT	CTC	AAC	ATG	ACC	TTT	TTC	TAT	TCG	6332
Ala	Ala	Gln	Thr	Gly	Leu	Thr	Ser	Leu	Asn	Met	Thr	Phe	Phe	Tyr	Ser	
			200					205					210			
CCT	AAA	AGA	ATA	GTA	AAC	GTC	ACG	TGG	ACA	ACC	GGC	GGC	CCC	TCC	CCC	6380
Pro	Lys	Arg	Ile	Val	Asn	Val	Thr	Trp	Thr	Thr	Gly	Gly	Pro	Ser	Pro	
		215					220					225				
TCG	CGC	ATA	ACG	GTA	TAC	TCG	TCG	CGG	GAG	AAC	GGG	CAG	CCC	GTG	TTG	6428
Ser	Arg	Ile	Thr	Val	Tyr	Ser	Ser	Arg	Glu	Asn	Gly	Gln	Pro	Val	Leu	
	230					235					240					
AGG	AAC	GTT	TCT	GAC	GGG	TTC	TTG	GTT	AAG	TAC	ACT	CCC	GAC	ATT	GAC	6476
Arg	Asn	Val	Ser	Asp	Gly	Phe	Leu	Val	Lys	Tyr	Thr	Pro	Asp	Ile	Asp	
245				250					255						260	
GGC	CGG	GCC	ATG	ATA	AAC	GTT	ATT	GCC	AAT	TAT	TCG	CCG	GCG	GAC	TCC	6524
Gly	Arg	Ala	Met	Ile	Asn	Val	Ile	Ala	Asn	Tyr	Ser	Pro	Ala	Asp	Ser	
			265					270						275		
GGC	AGC	GTC	CTC	GCG	TTT	ACG	GCC	TTT	AGG	GAA	GGA	AAA	CTC	CCA	TCC	6572
Gly	Ser	Val	Leu	Ala	Phe	Thr	Ala	Phe	Arg	Glu	Gly	Lys	Leu	Pro	Ser	
			280					285					290			
GCG	ATT	CAA	CTG	CAC	CGG	ATA	GAT	ATG	TCC	GGG	ACT	GAG	CCG	CCG	GGG	6620
Ala	Ile	Gln	Leu	His	Arg	Ile	Asp	Met	Ser	Gly	Thr	Glu	Pro	Pro	Gly	
		295					300					305				
ACT	GAA	ACG	ACC	TTC	GAC	TGT	CAA	AAA	ATG	ATA	GAA	ACC	CCG	TAC	CGA	6668
Thr	Glu	Thr	Thr	Phe	Asp	Cys	Gln	Lys	Met	Ile	Glu	Thr	Pro	Tyr	Arg	
	310					315					320					
GCG	CTC	GGG	AGC	AAT	GTT	CCC	AGG	GAC	GAC	TCT	ATC	CGT	CCG	GGG	GCC	6716
Ala	Leu	Gly	Ser	Asn	Val	Pro	Arg	Asp	Asp	Ser	Ile	Arg	Pro	Gly	Ala	
325				330						335					340	
ACT	CTG	CCT	CCG	TTC	GAT	ACC	GCA	GCA	CCT	GAT	TTC	GAT	ACA	GGT	ACT	6764
Thr	Leu	Pro	Pro	Phe	Asp	Thr	Ala	Ala	Pro	Asp	Phe	Asp	Thr	Gly	Thr	
				345					350					355		
TCC	CCG	ACC	CCC	ACT	ACC	GTG	CCA	GAG	CCA	GCC	ATT	ACT	ACA	CTC	ATA	6812
Ser	Pro	Thr	Pro	Thr	Thr	Val	Pro	Glu	Pro	Ala	Ile	Thr	Thr	Leu	Ile	
			360													

CCG	GCA	CAT	GAA	ACT	ACA	CAG	ACC	CAG	AGT	GCA	GAA	ACG	GTG	GTC	TTT	7052
Ala	Ala	His	Glu	Thr	Thr	Gln	Thr	Gln	Ser	Ala	Glu	Thr	Val	Val	Phe	
			440					445					450			
ACT	CAG	AGT	CCG	AGT	ACC	GAG	TCG	GAA	ACC	GCG	CGG	TCC	CAG	AGT	CAG	7100
Thr	Gln	Ser	Pro	Ser	Thr	Glu	Ser	Glu	Thr	Ala	Arg	Ser	Gln	Ser	Gln	
			455				460					465				
GAA	CCG	TGG	TAT	TTT	ACT	CAG	ACT	CCG	AGT	ACT	GAA	CAG	GCG	GCT	CTT	7148
Glu	Pro	Trp	Tyr	Phe	Thr	Gln	Thr	Pro	Ser	Thr	Glu	Gln	Ala	Ala	Leu	
			470				475					480				
ACT	CAG	ACG	CAG	ATC	GCA	GAA	ACG	GAG	GCG	TTG	TTT	ACT	CAG	ACT	CCG	7196
Thr	Gln	Thr	Gln	Ile	Ala	Glu	Thr	Glu	Ala	Leu	Phe	Thr	Gln	Thr	Pro	
					490					495					500	
AGT	GCT	GAA	CAG	ATG	ACT	TTT	ACT	CAG	ACT	CCG	GGT	GCA	GAA	ACC	GAG	7244
Ser	Ala	Glu	Gln	Met	Thr	Phe	Thr	Gln	Thr	Pro	Gly	Ala	Glu	Thr	Glu	
				505					510					515		
GCA	CCT	GCC	CAG	ACC	CCG	AGC	ACG	ATA	CCC	GAG	ATA	TTT	ACT	CAG	TCT	7292
Ala	Pro	Ala	Gln	Thr	Pro	Ser	Thr	Ile	Pro	Glu	Ile	Phe	Thr	Gln	Ser	
			520					525					530			
CGT	AGC	ACG	CCC	CCC	GAA	ACC	GCT	CGC	GCT	CCG	AGC	GCG	GCG	CCG	GAG	7340
Arg	Ser	Thr	Pro	Pro	Glu	Thr	Ala	Arg	Ala	Pro	Ser	Ala	Ala	Pro	Glu	
			535				540					545				
GTT	TTT	ACA	CAG	AGT	TCG	AGT	ACG	GTA	ACG	GAG	GTG	TTT	ACT	CAG	ACC	7388
Val	Phe	Thr	Gln	Ser	Ser	Ser	Thr	Val	Thr	Glu	Val	Phe	Thr	Gln	Thr	
			550				555				560					
CCG	AGC	ACG	GTA	CCG	AAA	ACT	ACT	CTG	AGT	TCG	AGT	ACT	GAA	CCG	GCG	7436
Pro	Ser	Thr	Val	Pro	Lys	Thr	Thr	Leu	Ser	Ser	Ser	Thr	Glu	Pro	Ala	
					570					575					580	
ATT	TTT	ACT	CGG	ACT	CAG	AGC	GCG	GGA	ACT	GAG	GCC	TTT	ACT	CAG	ACT	7484
Ile	Phe	Thr	Arg	Thr	Gln	Ser	Ala	Gly	Thr	Glu	Ala	Phe	Thr	Gln	Thr	
				585				590						595		
TCG	AGT	GCC	GAG	CCG	GAC	ACT	ATG	CGA	ACT	CAG	AGT	ACT	GAA	ACA	CAC	7532
Ser	Ser	Ala	Glu	Pro	Asp	Thr	Met	Arg	Thr	Gln	Ser	Thr	Glu	Thr	His	
			600					605					610			
TTT	TTC	ACT	CAG	GCC	CCG	AGT	ACG	GTA	CCG	AAA	GCT	ACT	CAG	ACT	CCG	7580
Phe	Phe	Thr	Gln	Ala	Pro	Ser	Thr	Val	Pro	Lys	Ala	Thr	Gln	Thr	Pro	
			615				620					625				
AGT	ACA	GAG	CCG	GAG	GTG	TTG	ACT	CAG	AGT	CCG	AGT	ACC	GAA	CCT	GTG	7628
Ser	Thr	Glu	Pro	Glu	Val	Leu	Thr	Gln	Ser	Pro	Ser	Thr	Glu	Pro	Val	
			630				635									

CCA	CAT	ACC	CAG	AAA	CTC	TAC	ACA	GAA	AAT	AAG	ACT	TTA	TCG	TTT	CCT	7868
Pro	His	Thr	Gln	Lys	Leu	Tyr	Thr	Glu	Asn	Lys	Thr	Leu	Ser	Phe	Pro	
	710					715						720				
ACT	GTT	GTT	TCA	GAA	TTC	CAT	GAG	ATG	TCG	ACG	GCA	GAG	TCG	CAG	ACG	7916
Thr	Val	Val	Ser	Glu	Phe	His	Glu	Met	Ser	Thr	Ala	Glu	Ser	Gln	Thr	
	725				730					735					740	
CCC	CTA	TTG	GAC	GTC	AAA	ATT	GTA	GAG	GTG	AAG	TTT	TCA	AAC	GAT	GGC	7964
Pro	Leu	Leu	Asp	Val	Lys	Ile	Val	Glu	Val	Lys	Phe	Ser	Asn	Asp	Gly	
				745					750					755		
GAA	GTA	ACG	GCG	ACT	TGC	GTT	TCC	ACC	GTC	AAA	TCT	CCC	TAT	AGG	GTA	8012
Glu	Val	Thr	Ala	Thr	Cys	Val	Ser	Thr	Val	Lys	Ser	Pro	Tyr	Arg	Val	
			760					765					770			
GAA	ACT	AAT	TGG	AAA	GTA	GAC	CTC	GTA	GAT	GTA	ATG	GAT	GAA	ATT	TCT	8060
Glu	Thr	Asn	Trp	Lys	Val	Asp	Leu	Val	Asp	Val	Met	Asp	Glu	Ile	Ser	
	775						780					785				
GGG	AAC	AGT	CCC	GCC	GGG	GTT	TTT	AAC	AGT	AAT	GAG	AAA	TGG	CAG	AAA	8108
Gly	Asn	Ser	Pro	Ala	Gly	Val	Phe	Asn	Ser	Asn	Glu	Lys	Trp	Gln	Lys	
	790					795					800					
CAG	CTG	TAC	TAC	AGA	GTA	ACC	GAT	GGA	AGA	ACA	TCG	GTC	CAG	CTA	ATG	8156
Gln	Leu	Tyr	Tyr	Arg	Val	Thr	Asp	Gly	Arg	Thr	Ser	Val	Gln	Leu	Met	
	805				810					815					820	
TGC	CTG	TCG	TGC	ACG	AGC	CAT	TCT	CCG	GAA	CCT	TAC	TGT	CTT	TTC	GAC	8204
Cys	Leu	Ser	Cys	Thr	Ser	His	Ser	Pro	Glu	Pro	Tyr	Cys	Leu	Phe	Asp	
				825					830					835		
ACG	TCT	CTT	ATA	GCG	AGG	GAA	AAA	GAT	ATC	GCG	CCA	GAG	TTA	TAC	TTT	8252
Thr	Ser	Leu	Ile	Ala	Arg	Glu	Lys	Asp	Ile	Ala	Pro	Glu	Leu	Tyr	Phe	
			840					845					850			
ACC	TCT	GAT	CCG	CAA	ACG	GCA	TAC	TGC	ACA	ATA	ACT	CTG	CCG	TCC	GGC	8300
Thr	Ser	Asp	Pro	Gln	Thr	Ala	Tyr	Cys	Thr	Ile	Thr	Leu	Pro	Ser	Gly	
		855					860					865				
GTT	GTT	CCG	AGA	TTC	GAA	TGG	AGC	CTT	AAT	AAT	GTT	TCA	CTG	CCG	GAA	8348
Val	Val	Pro	Arg	Phe	Glu	Trp	Ser	Leu	Asn	Asn	Val	Ser	Leu	Pro	Glu	
	870					875					880					
TAT	TTG	ACG	GCC	ACG	ACC	GTT	GTT	TCG	CAT	ACC	GCT	GGC	CAA	AGT	ACA	8396
Tyr	Leu	Thr	Ala	Thr	Thr	Val	Val	Ser	His	Thr	Ala	Gly	Gln	Ser	Thr	
	885				890					895					900	
GTG	TGG	AAG	AGC	AGC	GCG	AGA	GCA	GGC	GAG	GCG	TGG	ATT	TCT	GGC	CGG	8444
Val	Trp	Lys	Ser	Ser	Ala	Arg	Ala	Gly	Glu	Ala	Trp	Ile	Ser	Gly	Arg	
				905					910					915		
GGA	GGC	AAT	ATA													

ACC GCC ATT TAT TTT TGAGGAATGC TTTTGGACT ATCGTACTGC TTTCTTCCTT	8691
Thr Ala Ile Tyr Phe	
985	
CGCTAGCCAG AGCACCGCCG CCGTCACGTA CGACTACATT TTAGGCCGTC GCGCGCTCGA	8751
CGCGCTAACC ATACCGGCGG TTGGCCCGTA TAACAGATAC CTCACTAGGG TATCAAGAGG	8811
CTGCGACGTT GTCGAGCTCA ACCCGATTTC TAACGTGGAC GACATGATAT CGGCGGCCAA	8871
AGAAAAAGAG AAGGGGGGCC CTTTCGAGGC CTCCGTCGTC TGGTTCTACG TGATTAAGGG	8931
CGACGACGGC GAGGACAAAGT ACTGTCCAAT CTATAGAAAA GAGTACAGGG AATGTGGCGA	8991
CGTACAACCTG CTATCTGAAT GCGCCGTTCA ATCTGCACAG ATGTGGGCAG TGGACTATGT	9051
TCCTAGCACC CTTGTATCGC GAAATGGCGC GGGACTGACT ATATTCTCCC CCACTGCTGC	9111
GCTCTCTGGC CAATACTTGC TGACCCTGAA AATCGGGAGA TTTGCGCAA CAGCTCTCGT	9171
AACTCTAGAA GTTAACGATC GCTGTTTAAA GATCGGGTCG CAGCTTAACT TTTTACCGTC	9231
GAAATGCTGG ACAACAGAAC AGTATCAGAC TGGATTTCAG GCGAACACC TTTATCCGAT	9291
CGCAGACACC AATACACGAC ACGCGGACGA CGTATATCGG GGATACGAAG ATATTCTGCA	9351
GCGCTGGAAT AATTTGCTGA GGAAAAAGAA TCCTAGCGCG CCAGACCCCTC GTCCAGATAG	9411
CGTCCCGCAA GAAATTCCCG CTGTAACCAA GAAAGCGGAA GGGCGCACCC CGGACGCAGA	9471
AAGCAGCGAA AAGAAGGCCC CTCCAGAAGA CTCGGAGGAC GACATGCAGG CAGAGGCTTC	9531
TGGAGAAAAT CCTGCCGCCC TCCCCGAAGA CGACGAAGTC CCCGAGGACA CCGAGCACGA	9591
TGATCCAAAC TCGGATCCTG ACTATTACAA TGACATGCCC GCCGTGATCC CGGTGGAGGA	9651
GACTACTAAA AGTTCTAATG CCGTCTCCAT GCCCATATTC GCGGCGTTTC TAGCCTGCGC	9711
GGTCGCGCTC GTGGGGCTAC TGGTTTGGAG CATCGTAAAA TGCGCGCGTA GCTAATCGAG	9771
CCTAGAATAG GTGGTTTCTT CCTACATGCC ACGCCTCACG CTCATAATAT AAATCACATG	9831
GAATAGCATA CCAATGCCTA TTCATTGGGA CGTTCGAAAA GC	9873
ATG GCA TCG CTA CTT GGA ACT	9894
Met Ala Ser Leu Leu Gly Thr	
1 5	
CTG GCT CTC CTT GCC GCG ACG CTC GCA CCC TTC GGC GCG ATG GGA ATC	9942
Leu Ala Leu Leu Ala Ala Thr Leu Ala Pro Phe Gly Ala Met Gly Ile	
10 15 20	
GTG ATC ACT GGA AAT CAC GTC TCC GCC AGG ATT GAC GAC GAT CAC ATC	9990
Val Ile Thr Gly Asn His Val Ser Ala Arg Ile Asp Asp Asp His Ile	
25 30 35	
GTG ATC GTC GCG CCT CGC CCC GAA GCT ACA ATT CAA CTG CAG CTA TTT	10038
Val Ile Val Ala Pro Arg Pro Glu Ala Thr Ile Gln Leu Gln Leu Phe	
40 45 50 55	
TTC ATG CCT GGC CAG AGA CCC CAC AAA CCC TAC TCA GGA ACC GTC CGC	10086
Phe Met Pro Gly Gln Arg Pro His Lys Pro Tyr Ser Gly Thr Val Arg	
60 65 70	
GTC GCG TTT CGG TCT GAT ATA ACA AAC CAG TGC TAC CAG GAA CTT AGC	10134
Val Ala Phe Arg Ser Asp Ile Thr Asn Gln Cys Tyr Gln Glu Leu Ser	
75 80 85	

GAG	GAG	CGC	TTT	GAA	AAT	TGC	ACT	CAT	CGA	TCG	TCT	TCT	GTT	TTT	GTC	10182
Glu	Glu	Arg	Phe	Glu	Asn	Cys	Thr	His	Arg	Ser	Ser	Ser	Val	Phe	Val	
		90					95						100			
GGC	TGT	AAA	GTG	ACC	GAG	TAC	ACG	TTC	TCC	GCC	TCG	AAC	AGA	CTA	ACC	10230
Gly	Cys	Lys	Val	Thr	Glu	Tyr	Thr	Phe	Ser	Ala	Ser	Asn	Arg	Leu	Thr	
	105					110					115					
GGA	CCT	CCA	CAC	CCG	TTT	AAG	CTC	ACT	ATA	CGA	AAT	CCT	CGT	CCG	AAC	10278
Gly	Pro	Pro	His	Pro	Phe	Lys	Leu	Thr	Ile	Arg	Asn	Pro	Arg	Pro	Asn	
120					125					130					135	
GAC	AGC	GGG	ATG	TTC	TAC	GTA	ATT	GTT	CGG	CTA	GAC	GAC	ACC	AAA	GAA	10326
Asp	Ser	Gly	Met	Phe	Tyr	Val	Ile	Val	Arg	Leu	Asp	Asp	Thr	Lys	Glu	
			140						145					150		
CCC	ATT	GAC	GTC	TTC	GCG	ATC	CAA	CTA	TCG	GTG	TAT	CAA	TTC	GCG	AAC	10374
Pro	Ile	Asp	Val	Phe	Ala	Ile	Gln	Leu	Ser	Val	Tyr	Gln	Phe	Ala	Asn	
		155						160					165			
ACC	GCC	GCG	ACT	CGC	GGA	CTC	TAT	TCC	AAG	GCT	TCG	TGT	CGC	ACC	TTC	10422
Thr	Ala	Ala	Thr	Arg	Gly	Leu	Tyr	Ser	Lys	Ala	Ser	Cys	Arg	Thr	Phe	
	170					175						180				
GGA	TTA	CCT	ACC	GTC	CAA	CTT	GAG	GCC	TAT	CTC	AGG	ACC	GAG	GAA	AGT	10470
Gly	Leu	Pro	Thr	Val	Gln	Leu	Glu	Ala	Tyr	Leu	Arg	Thr	Glu	Glu	Ser	
	185					190					195					
TGG	CGC	AAC	TGG	CAA	GCG	TAC	GTT	GCC	ACG	GAG	GCC	ACG	ACG	ACC	AGC	10518
Trp	Arg	Asn	Trp	Gln	Ala	Tyr	Val	Ala	Thr	Glu	Ala	Thr	Thr	Thr	Ser	
200				205						210					215	
GCC	GAG	GCG	ACA	ACC	CCG	ACG	CCC	GTC	ACT	GCA	ACC	AGC	GCC	TCC	GAA	10566
Ala	Glu	Ala	Thr	Thr	Pro	Thr	Pro	Val	Thr	Ala	Thr	Ser	Ala	Ser	Glu	
			220					225						230		
CTT	GAA	GCG	GAA	CAC	TTT	ACC	TTT	CCC	TGG	CTA	GAA	AAT	GGC	GTG	GAT	10614
Leu	Glu	Ala	Glu	His	Phe	Thr	Phe	Pro	Trp	Leu	Glu	Asn	Gly	Val	Asp	
		235						240					245			
CAT	TAC	GAA	CCG	ACA	CCC	GCA	AAC	GAA	AAT	TCA	AAC	GTT	ACT	GTC	CGT	10662
His	Tyr	Glu	Pro	Thr	Pro	Ala	Asn	Glu	Asn	Ser	Asn	Val	Thr	Val	Arg	
	250					255						260				
CTC	GGG	ACA	ATG	AGC	CCT	ACG	CTA	ATT	GGG	GTA	ACC	GTG	GCT	GCC	GTC	10710
Leu	Gly	Thr	Met	Ser	Pro	Thr	Leu	Ile	Gly	Val	Thr	Val	Ala	Ala	Val	
	265					270					275					
GTG	AGC	GCA	ACG	ATC	GGC	CTC	GTC	ATT	GTA	ATT	TCC	ATC	GTC	ACC	AGA	10758
Val	Ser	Ala	Thr	Ile	Gly	Leu	Val	Ile	Val	Ile	Ser	Ile	Val	Thr	Arg	
280					285					290					295	
AAC	ATG	TGC	ACC	CCG	CAC	CGA	AAA	TTA	GAC	ACG	GTC	TCG	CAA	GAC	GAC	10806
Asn	Met	Cys	Thr	Pro	His	Arg	Lys	Leu	Asp	Thr	Val	Ser	Gln	Asp	Asp	
			300					305						310		
GAA	GAA	CGT	TCC	CAA	ACT	AGA	AGG	GAA	TCG	CGA	AAA	TTT	GGA	CCC	ATG	10854
Glu	Glu	Arg	Ser	Gln	Thr	Arg	Arg	Glu	Ser	Arg	Lys	Phe	Gly	Pro	Met	
		315						320					325			
GTT	GCG	TGC	GAA	ATA	AAC	AAG	GGC	GCT	GAC	CAG	GAT	AGT	GAA	CTT	GTG	10902
Val	Ala	Cys	Glu	Ile	Asn	Lys	Gly	Ala	Asp	Gln	Asp	Ser	Glu	Leu	Val	
	330					335						340				
GAA	CTG	GTT	GCG	ATT	GTT	AAC	CCG	TCT	GCG	CTA	AGC	TCG	CCC	GAC	TCA	10950
Glu	Leu	Val	Ala	Ile	Val	Asn	Pro	Ser	Ala	Leu	Ser	Ser	Pro	Asp	Ser	
	345					350					355					

10182 10230 10278 10326 10374 10422 10470 10518 10566 10614 10662 10710 10758 10806 10854 10902 10950

ATA AAA ATG TGATTAAGTC TGAATGTGGC TCTCCAATCA TTTCGATTCT Ile Lys Met 360	10999
CTAATCTCCC AATCCTCTCA AAAGGGGCAG TATCGGACAC GGACTGGGAG GGGCGTACTA	11059
CACGATAGTT ATATGGTACA GCAGAGGCCT CTGAACACTT AGGAGGAGAA TTCAGCCGGG	11119
GAGAGCCCCCT GTTGAGTAGG CTTGGGAGCA TATTGCAGG ATG AAC ATG TTA GTG Met Asn Met Leu Val 1 5	11173
ATA GTT CTC GCC TCT TGT CTT GCG CGC CTA ACT TTT GCG ACG CGA CAC Ile Val Leu Ala Ser Cys Leu Ala Arg Leu Thr Phe Ala Thr Arg His 10 15 20	11221
GTC CTC TTT TTG GAA GGC ACT CAG GCT GTC CTC GGG GAA GAT GAT CCC Val Leu Phe Leu Glu Gly Thr Gln Ala Val Leu Gly Glu Asp Asp Pro 25 30 35	11269
AGA AAC GTT CCG GAA GGG ACT GTA ATC AAA TGG ACA AAA GTC CTG CGG Arg Asn Val Pro Glu Gly Thr Val Ile Lys Trp Thr Lys Val Leu Arg 40 45 50	11317
AAC GCG TGC AAG ATG AAG GCG GCC GAT GTC TGC TCT TCG CCT AAC TAT Asn Ala Cys Lys Met Lys Ala Ala Asp Val Cys Ser Ser Pro Asn Tyr 55 60 65	11365
TGC TTT CAT GAT TTA ATT TAC GAC GGA GGA AAG AAA GAC TGC CCG CCC Cys Phe His Asp Leu Ile Tyr Asp Gly Gly Lys Lys Asp Cys Pro Pro 70 75 80 85	11413
GCG GGA CCC CTG TCT GCA AAC CTG GTA ATT TTA CTA AAG CGC GGC GAA Ala Gly Pro Leu Ser Ala Asn Leu Val Ile Leu Leu Lys Arg Gly Glu 90 95 100	11461
AGC TTC GTC GTG CTG GGT TCT GGG CTA CAC AAC AGC AAT ATA ACT AAT Ser Phe Val Val Leu Gly Ser Gly Leu His Asn Ser Asn Ile Thr Asn 105 110 115	11509
ATC ATG TGG ACA GAG TAC GGA GGC CTG CTC TTT GAT CCT GTA ACT CGT Ile Met Trp Thr Glu Tyr Gly Gly Leu Leu Phe Asp Pro Val Thr Arg 120 125 130	11557
TCG GAC GAG GGA ATC TAT TTT CGA CGG ATC TCT CAG CCA GAT CTG GCC Ser Asp Glu Gly Ile Tyr Phe Arg Arg Ile Ser Gln Pro Asp Leu Ala 135 140 145	11605
ATG GAA ACT ACA TCG TAC AAC GTC AGC GTT CTT TCG CAC GTA GAC GAG Met Glu Thr Thr Ser Tyr Asn Val Ser Val Leu Ser His Val Asp Glu 150 155 160 165	11653
AAG GCT CCA GCA CCG CAC GAG GTG GAG ATA GAC ACC ATC AAG CCG TCA Lys Ala Pro Ala Pro His Glu Val Glu Ile Asp Thr Ile Lys Pro Ser 170 175 180	11701
GAG GCC CAC GCG CAC GTG GAA TTA CAA ATG CTG CCG TTT CAT GAA CTC Glu Ala His Ala His Val Glu Leu Gln Met Leu Pro Phe His Glu Leu 185 190 195	11749
AAC GAC AAC AGC CCC ACC TAT GTG ACC CCT GTT CTT AGA GTC TTC CCA Asn Asp Asn Ser Pro Thr Tyr Val Thr Pro Val Leu Arg Val Phe Pro 200 205 210	11797
CCG ACC GAG CAC GTA AAA TTT AAC GTT ACG TAT TCG TGG TAT GGG TTT Pro Thr Glu His Val Lys Phe Asn Val Thr Tyr Ser Trp Tyr Gly Phe 215 220 225	11845

GAT GTC AAA GAG GAG TGC GAA GAA GTG AAA CTG TTC GAG CCG TGC GTA Asp Val Lys Glu Glu Cys Glu Glu Val Lys Leu Phe Glu Pro Cys Val 230 235 240 245	11893
TAC CAT CCT ACA GAC GGC AAA TGT CAG TTT CCC GCA ACC AAC CAG AGA Tyr His Pro Thr Asp Gly Lys Cys Gln Phe Pro Ala Thr Asn Gln Arg 250 255 260	11941
TGC CTC ATA GGA TCT GTC TTG ATG GCG GAA TTC TTG GGC GCG GCC TCT Cys Leu Ile Gly Ser Val Leu Met Ala Glu Phe Leu Gly Ala Ala Ser 265 270 275	11989
TTG CTG GAT TGT TCC CGC GAT ACT CTA GAA GAC TGC CAC GAA AAT CGC Leu Leu Asp Cys Ser Arg Asp Thr Leu Glu Asp Cys His Glu Asn Arg 280 285 290	12037
GTG CCG AAC CTA CGG TTC GAT TCG CGA CTC TCC GAG TCA CGC GCA GGC Val Pro Asn Leu Arg Phe Asp Ser Arg Leu Ser Glu Ser Arg Ala Gly 295 300 305	12085
CTG GTG ATC AGT CCT CTT ATA GCC ATC CCC AAA GTT TTG ATT ATA GTC Leu Val Ile Ser Pro Leu Ile Ala Ile Pro Lys Val Leu Ile Ile Val 310 315 320 325	12133
GTT TCC GAC GGA GAC ATT TTG GGA TGG AGC TAC ACG GTG CTC GGG AAA Val Ser Asp Gly Asp Ile Leu Gly Trp Ser Tyr Thr Val Leu Gly Lys 330 335 340	12181
CGT AAC AGT CCG CGC GTA GTA GTC GAA ACG CAC ATG CCC TCG AAG GTC Arg Asn Ser Pro Arg Val Val Val Glu Thr His Met Pro Ser Lys Val 345 350 355	12229
CCG ATG AAC AAA GTA GTA ATT GGC AGT CCC GGA CCA ATG GAC GAA ACG Pro Met Asn Lys Val Val Ile Gly Ser Pro Gly Pro Met Asp Glu Thr 360 365 370	12277
GGT AAC TAT AAA ATG TAC TTC GTC GTC GCG GGG GTG GCC GCG ACG TGC Gly Asn Tyr Lys Met Tyr Phe Val Val Ala Gly Val Ala Ala Thr Cys 375 380 385	12325
GTA ATT CTT ACA TGC GCT CTG CTT GTG GGG AAA AAG AAG TGC CCC GCG Val Ile Leu Thr Cys Ala Leu Leu Val Gly Lys Lys Lys Cys Pro Ala 390 395 400 405	12373
CAC CAA ATG GGT ACT TTT TCC AAG ACC GAA CCA TTG TAC GCG CCG CTC His Gln Met Gly Thr Phe Ser Lys Thr Glu Pro Leu Tyr Ala Pro Leu 410 415 420	12421
CCC AAA AAC GAG TTT GAG GCC GGC GGG CTT ACG GAC GAT GAG GAA GTG Pro Lys Asn Glu Phe Glu Ala Gly Gly Leu Thr Asp Asp Glu Glu Val 425 430 435	12469
ATT TAT GAC GAA GTA TAC GAA CCC CTA TTT CGC GGC TAC TGT AAG CAG Ile Tyr Asp Glu Val Tyr Glu Pro Leu Phe Arg Gly Tyr Cys Lys Gln 440 445 450	12517
GAA TTC CGC GAA GAT GTG AAT ACC TTT TTC GGT GCG GTC GTG GAG GGA Glu Phe Arg Glu Asp Val Asn Thr Phe Phe Gly Ala Val Val Glu Gly 455 460 465	12565
GAA AGG GCC TTA AAC TTT AAA TCC GCC ATC GCA TCA ATG GCA GAT CGC Glu Arg Ala Leu Asn Phe Lys Ser Ala Ile Ala Ser Met Ala Asp Arg 470 475 480 485	12613
ATC CTG GCA AAT AAA AGC GGC AGA AGG AAT ATG GAT AGC TAT TAGTTGGTC Ile Leu Ala Asn Lys Ser Gly Arg Arg Asn Met Asp Ser Tyr 490 495 500	12664

ATG CCT TTT AAG ACC AGA GGG GCC GAA GAC	12694
Met Pro Phe Lys Thr Arg Gly Ala Glu Asp	
1 5 10	
GCG GCC GCG GGC AAG AAC AGG TTT AAG AAA TCG AGA AAT CGG GAA ATC	12742
Ala Ala Ala Gly Lys Asn Arg Phe Lys Lys Ser Arg Asn Arg Glu Ile	
15 20 25	
TTA CCG ACC AGA CTG CGT GGC ACC GGT AAG AAA ACT GCC GGA TTG TCC	12790
Leu Pro Thr Arg Leu Arg Gly Thr Gly Lys Lys Thr Ala Gly Leu Ser	
30 35 40	
AAT TAT ACC CAG CCT ATT CCC TGG AAC CCT AAA TTC TGC AGC GCG CGC	12838
Asn Tyr Thr Gln Pro Ile Pro Trp Asn Pro Lys Phe Cys Ser Ala Arg	
45 50 55	
GGG GAA TCT GAC AAC CAC GCG TGT AAA GAC ACT TTT TAT CGC AGG ACG	12886
Gly Glu Ser Asp Asn His Cys Lys Asp Thr Tyr Arg Arg Thr	
60 65 70	
TGC TGC GCA TCG CGC TCT ACC GTT TCC AGT CAA CCC GAT TCC CCC CAC	12934
Cys Cys Ala Ser Arg Ser Thr Val Ser Ser Gln Pro Asp Ser Pro His	
75 80 85 90	
ACA CCC ATG CCT ACT GAG TAT GGG CGC GTG CCC TCC GCA AAG CGC AAA	12982
Thr Pro Met Pro Thr Glu Tyr Gly Arg Val Pro Ser Ala Lys Arg Lys	
95 100 105	
AAA CTA TCA TCT TCA GAC TSS GAG GGC GCG CAC CAA CCC CTA GTA TCC	13030
Lys Leu Ser Ser Ser Asp Xaa Glu Gly Ala His Gln Pro Leu Val Ser	
110 115 120	
TGT AAA CTT CCG GAT TCT CAA GCA GCA CCG GCG CGA ACC TAT AGT TCT	13078
Cys Lys Leu Pro Asp Ser Gln Ala Ala Pro Ala Arg Thr Tyr Ser Ser	
125 130 135	
GCG CAA AGA TAT ACT GTT GAC GAG GTT TCG TCG CCA ACT CCG CCA GGC	13126
Ala Gln Arg Tyr Thr Val Asp Glu Val Ser Ser Pro Thr Pro Pro Gly	
140 145 150	
GTC GAC GCT GTT GCG GAC TTA GAA ACG CGC GCG GAA CTT CCT GGC GCT	13174
Val Asp Ala Val Ala Asp Leu Glu Thr Arg Ala Glu Leu Pro Gly Ala	
155 160 165 170	
ACG ACG GAA CAA ACG GAA AGT AAA AAT AAG CTC CCC AAC CAA CAA TCG	13222
Thr Thr Glu Gln Thr Glu Ser Lys Asn Lys Leu Pro Asn Gln Gln Ser	
175 180 185	
CGC CTG AAG CCG AAA CCC ACA AAC GAG CAC GTC GGA GGG GAG CGG TGC	13270
Arg Leu Lys Pro Lys Pro Thr Asn Glu His Val Gly Gly Glu Arg Cys	
190 195 200	
CCC TCC GAA GGC ACG GTC GAG GCG CCA TCG CTC GGC ATC CTC TCG CGC	13318
Pro Ser Glu Gly Thr Val Glu Ala Pro Ser Leu Gly Ile Leu Ser Arg	
205 210 215	
GTC GGG GCA GCG ATA GCA AAC GAG CTG GCT CGT ATG CGG AGG GCG TGT	13366
Val Gly Ala Ala Ile Ala Asn Glu Leu Ala Arg Met Arg Arg Ala Cys	
220 225 230	
CTT CCG CTC GCC GCG TCG GCG GCC GCT GCC GGA ATA GTG GCC TGG GCC	13414
Leu Pro Leu Ala Ala Ser Ala Ala Ala Ala Gly Ile Val Ala Trp Ala	
235 240 245 250	
GCG GCG AGG GCC TTG CAG AAA CAA GGG CGG TAG CAGTAATAATA ACCACACAA	13467
Ala Ala Arg Ala Leu Gln Lys Gln Gly Arg *	
255 260	

12694 12742 12790 12838 12886 12934 12982 13030 13078 13126 13174 13222 13270 13318 13366 13414 13467

ATATTG

13473

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 476 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Arg Phe Arg Arg Ile Cys Ser Arg Ser Arg Ala Glu Lys Arg Arg
 1 5 10 15
 Arg Thr Thr Glu Asn Pro Leu Thr Ser Lys Arg Val Cys Val Leu Asp
 20 25 30
 Ser Phe Ser Arg Thr Met Ser Leu Arg Pro Tyr Ala Glu Ile Leu Pro
 35 40 45
 Thr Ala Glu Gly Val Glu Arg Leu Ala Glu Leu Val Ser Val Thr Met
 50 55 60
 Thr Glu Arg Ala Glu Pro Val Thr Glu Asn Thr Ala Val Asn Ser Ile
 65 70 75 80
 Pro Pro Ala Asn Glu Asn Gly Gln Asn Phe Ala Tyr Ala Gly Asp Gly
 85 90 95
 Pro Ser Thr Thr Glu Lys Val Asp Gly Ser His Thr Asp Phe Asp Glu
 100 105 110
 Ala Ser Ser Asp Tyr Ala Gly Pro Val Pro Leu Ala Gln Thr Arg Leu
 115 120 125
 Lys His Ser Asp Glu Phe Leu Gln His Phe Arg Val Leu Asp Asp Leu
 130 135 140
 Val Glu Gly Ala Tyr Gly Phe Ile Cys Gly Val Arg Arg Tyr Thr Glu
 145 150 155 160
 Glu Glu Gln Arg Arg Arg Gly Val Asn Ser Thr Asn Gln Gly Lys Ser
 165 170 175
 Lys Cys Lys Arg Leu Ile Ala Lys Tyr Val Lys Asn Gly Thr Arg Ala
 180 185 190
 Ala Ser Gln Leu Glu Asn Glu Ile Leu Val Leu Gly Arg Leu Asn His
 195 200 205
 Glu Asn Val Leu Lys Ile Gln Glu Ile Leu Arg Tyr Pro Asp Asn Thr
 210 215 220
 Tyr Met Leu Thr Gln Arg Tyr Gln Phe Asp Leu Tyr Ser Tyr Met Tyr
 225 230 235 240
 Asp Glu Ala Phe Asp Trp Lys Asp Ser Pro Met Leu Lys Gln Thr Arg
 245 250 255
 Arg Ile Met Lys Gln Leu Met Ser Ala Val Ser Tyr Ile His Ser Lys
 260 265 270

Lys Leu Ile His Arg Asp Ile Lys Leu Glu Asn Ile Phe Leu Asn Cys
 275 280 285
 Asp Gly Lys Thr Val Leu Gly Asp Phe Gly Thr Val Thr Pro Phe Glu
 290 295 300
 Asn Glu Arg Glu Pro Phe Glu Tyr Gly Trp Val Gly Thr Val Ala Thr
 305 310 315 320
 Asn Ser Pro Glu Ile Leu Ala Arg Asp Ser Tyr Cys Glu Ile Thr Asp
 325 330 335
 Ile Trp Ser Cys Gly Val Val Leu Leu Glu Met Val Ser His Glu Phe
 340 345 350
 Cys Pro Ile Gly Asp Gly Gly Gly Asn Pro His Gln Gln Leu Leu Lys
 355 360 365
 Val Ile Asp Ser Leu Ser Val Cys Asp Glu Glu Phe Pro Asp Pro Pro
 370 375 380
 Cys Asn Leu Tyr Asn Tyr Leu His Tyr Ala Ser Ile Asp Arg Ala Gly
 385 390 395 400
 His Thr Val Pro Ser Leu Ile Arg Asn Leu His Leu Pro Ala Asp Val
 405 410 415
 Glu Tyr Pro Leu Val Lys Met Leu Thr Phe Asp Trp Arg Leu Arg Pro
 420 425 430
 Ser Ala Ala Glu Val Leu Ala Met Pro Leu Phe Ser Ala Glu Glu Glu
 435 440 445
 Arg Thr Ile Thr Ile Ile His Gly Lys His Lys Pro Ile Arg Pro Glu
 450 455 460
 Ile Arg Ala Arg Val Pro Arg Ser Met Ser Glu Gly
 465 470 475

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 510 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Thr Leu Pro His Arg Leu Thr Lys Arg Pro Phe Ala Arg Arg Phe
 1 5 10 15
 Cys Ser Val Phe Val Ile His Tyr Ser Glu Thr Lys Leu Asp Arg Tyr
 20 25 30
 Asn Lys Thr Met Leu Leu Tyr Arg Pro Asp Ser Thr Met Arg His Ser
 35 40 45
 Gly Gly Asp Ala Asn His Arg Gly Ile Arg Pro Arg Arg Lys Ser Ile
 50 55 60
 Gly Ala Phe Ser Ala Arg Glu Lys Thr Gly Lys Arg Asn Ala Leu Thr
 65 70 75 80

Glu Ser Ser Ser Ser Ser Asp Met Leu Asp Pro Phe Ser Thr Asp Lys
 85 90 95
 Glu Phe Gly Gly Lys Trp Thr Val Asp Gly Pro Ala Asp Ile Thr Ala
 100 105 110
 Glu Val Leu Ser Gln Ala Trp Asp Val Leu Gln Leu Val Lys His Glu
 115 120 125
 Asp Ala Glu Glu Glu Arg Val Thr Tyr Glu Ser Lys Pro Thr Pro Ile
 130 135 140
 Gln Pro Phe Asn Ala Trp Pro Asp Gly Pro Ser Trp Asn Ala Gln Asp
 145 150 155 160
 Phe Thr Arg Ala Pro Ile Val Tyr Pro Ser Ala Glu Val Leu Asp Ala
 165 170 175
 Glu Ala Leu Lys Val Gly Ala Phe Val Ser Arg Val Leu Gln Cys Val
 180 185 190
 Pro Phe Thr Arg Ser Lys Lys Ser Val Thr Val Arg Asp Ala Gln Ser
 195 200 205
 Phe Leu Gly Asp Ser Phe Trp Arg Ile Met Gln Asn Val Tyr Thr Val
 210 215 220
 Cys Leu Arg Gln His Ile Thr Arg Leu Arg His Pro Ser Ser Lys Ser
 225 230 235 240
 Ile Val Asn Cys Asn Asp Pro Leu Trp Tyr Ala Tyr Ala Asn Gln Phe
 245 250 255
 His Trp Arg Gly Met Arg Val Pro Ser Leu Lys Leu Ala Ser Pro Pro
 260 265 270
 Glu Glu Asn Ile Gln His Gly Pro Met Ala Ala Val Phe Arg Asn Ala
 275 280 285
 Gly Ala Gly Leu Phe Leu Trp Pro Ala Met Arg Ala Ala Phe Glu Glu
 290 295 300
 Arg Asp Lys Arg Leu Leu Arg Ala Cys Leu Ser Ser Leu Asp Ile Met
 305 310 315 320
 Asp Ala Ala Val Leu Ala Ser Phe Pro Phe Tyr Trp Arg Gly Val Gln
 325 330 335
 Asp Thr Ser Arg Phe Glu Pro Ala Leu Gly Cys Leu Ser Glu Tyr Phe
 340 345 350
 Ala Leu Val Val Leu Leu Ala Glu Thr Val Leu Ala Thr Met Phe Asp
 355 360 365
 His Ala Leu Val Phe Met Arg Ala Leu Ala Asp Gly Asn Phe Asp Asp
 370 375 380
 Tyr Asp Glu Thr Arg Tyr Ile Asp Pro Val Lys Asn Glu Tyr Leu Asn
 385 390 395 400
 Gly Ala Glu Gly Thr Leu Leu Arg Gly Ile Val Ala Ser Asn Thr Ala
 405 410 415
 Leu Ala Val Val Cys Ala Asn Thr Tyr Ser Thr Ile Arg Lys Leu Pro
 420 425 430

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Ser Val Ala Thr Ser Ala Cys Asn Val Ala Tyr Arg Thr Glu Thr Leu
435 440 445
Lys Ala Arg Arg Pro Gly Met Ser Asp Ile Tyr Arg Ile Leu Gln Lys
450 455 460
Glu Phe Phe Phe Tyr Ile Ala Trp Leu Gln Arg Val Ala Thr His Ala
465 470 475 480
Asn Phe Cys Leu Asn Ile Leu Lys Arg Ser Val Asp Thr Gly Pro Arg
485 490 495
His Phe Cys Ser Gly Pro Ala Arg Arg Ser Gly Cys Ser Ser
500 505 510

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 110 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Leu Cys Pro Leu Leu Val Pro Ile Gln Tyr Glu Asp Phe Ser Lys
1 5 10 15
Ala Met Gly Ser Glu Leu Lys Arg Glu Lys Leu Glu Thr Phe Val Lys
20 25 30
Ala Ile Ser Ser Asp Arg Asp Pro Arg Gly Ser Leu Arg Phe Leu Ile
35 40 45
Ser Asp His Ala Arg Glu Ile Ile Ala Asp Gly Val Arg Phe Lys Pro
50 55 60
Val Ile Asp Glu Pro Val Arg Ala Ser Val Ala Leu Ser Thr Ala Ala
65 70 75 80
Ala Gly Lys Val Lys Ala Arg Arg Leu Thr Ser Val Arg Ala Pro Val
85 90 95
Pro Pro Ala Gly Ala Val Ser Ala Arg Arg Lys Ser Glu Ile
100 105 110

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 292 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ser Gly Phe Ser Asn Ile Gly Ser Ile Ala Thr Val Ser Leu Val
1 5 10 15
Cys Ser Leu Leu Cys Ala Ser Val Leu Gly Ala Pro Val Leu Asp Gly
20 25 30

Leu Glu Ser Ser Pro Phe Pro Phe Gly Gly Lys Ile Ile Ala Gln Ala
35 40 45

Cys Asn Arg Thr Thr Ile Glu Val Thr Val Pro Trp Ser Asp Tyr Ser
50 55 60

Gly Arg Thr Glu Gly Val Ser Val Glu Val Lys Trp Phe Tyr Gly Asn
65 70 75 80

Ser Asn Pro Glu Ser Phe Val Phe Gly Val Asp Ser Glu Thr Gly Ser
85 90 95

Gly His Glu Asp Leu Ser Thr Cys Trp Ala Leu Ile His Asn Leu Asn
100 105 110

Ala Ser Val Cys Arg Ala Ser Asp Ala Gly Ile Pro Asp Phe Asp Lys
115 120 125

Gln Cys Glu Lys Val Gln Arg Arg Leu Arg Ser Gly Val Glu Leu Gly
130 135 140

Ser Tyr Val Ser Gly Asn Gly Ser Leu Val Leu Tyr Pro Gly Met Tyr
145 150 155 160

Asp Ala Gly Ile Tyr Ala Tyr Gln Leu Ser Val Gly Gly Lys Gly Tyr
165 170 175

Thr Gly Ser Val Tyr Leu Asp Val Gly Pro Asn Pro Gly Cys His Asp
180 185 190

Gln Tyr Gly Tyr Thr Tyr Tyr Ser Leu Ala Asp Glu Ala Ser Asp Leu
195 200 205

Ser Ser Tyr Asp Val Ala Ser Pro Glu Leu Asp Gly Pro Met Glu Glu
210 215 220

Asp Tyr Ser Asn Cys Leu Asp Met Pro Pro Leu Arg Pro Trp Thr Thr
225 230 235 240

Val Cys Ser His Asp Val Glu Glu Gln Glu Asn Ala Thr Asp Glu Leu
245 250 255

Tyr Leu Trp Asp Glu Glu Cys Ala Gly Pro Leu Asp Glu Tyr Val Asp
260 265 270

Glu Arg Ser Glu Thr Met Pro Arg Met Val Val Phe Ser Pro Pro Ser
275 280 285

Thr Leu Gln Gln
290

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 985 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gly Thr Met Leu Val Leu Arg Leu Phe Leu Leu Ala Val Ala Asp
1 5 10 15

Ala Ala Leu Pro Thr Gly Arg Phe Cys Arg Val Trp Lys Val Pro Pro
20 25 30

Gly Gly Thr Ile Gln Glu Asn Leu Ala Val Leu Ala Glu Ser Pro Val
35 40 45

Thr Gly His Ala Thr Tyr Pro Pro Pro Glu Gly Ala Val Ser Phe Gln
50 55 60

Ile Phe Ala Asp Thr Pro Thr Leu Arg Ile Arg Tyr Gly Pro Thr Glu
65 70 75 80

Asp Glu Leu Ala Leu Glu Arg Gly Thr Ser Ala Ser Asp Ala Asp Asn
85 90 95

Val Thr Phe Ser Leu Ser Tyr Arg Pro Arg Pro Glu Ile His Gly Ala
100 105 110

Tyr Phe Thr Ile Gly Val Phe Ala Thr Gly Gln Ser Thr Glu Ser Ser
115 120 125

Tyr Ser Val Ile Ser Arg Val Leu Val Asn Ala Ser Leu Glu Arg Ser
130 135 140

Val Arg Leu Glu Thr Pro Cys Asp Glu Asn Phe Leu Gln Asn Glu Pro
145 150 155 160

Thr Trp Gly Ser Lys Arg Trp Leu Gly Pro Pro Ser Pro Tyr Val Arg
165 170 175

Asp Asn Asp Val Ala Val Leu Thr Lys Ala Gln Tyr Ile Gly Glu Cys
180 185 190

Tyr Ser Asn Ser Ala Ala Gln Thr Gly Leu Thr Ser Leu Asn Met Thr
195 200 205

Phe Phe Tyr Ser Pro Lys Arg Ile Val Asn Val Thr Trp Thr Thr Gly
210 215 220

Gly Pro Ser Pro Ser Arg Ile Thr Val Tyr Ser Ser Arg Glu Asn Gly
225 230 235 240

Gln Pro Val Leu Arg Asn Val Ser Asp Gly Phe Leu Val Lys Tyr Thr
245 250 255

Pro Asp Ile Asp Gly Arg Ala Met Ile Asn Val Ile Ala Asn Tyr Ser
260 265 270

Pro Ala Asp Ser Gly Ser Val Leu Ala Phe Thr Ala Phe Arg Glu Gly
275 280 285

Lys Leu Pro Ser Ala Ile Gln Leu His Arg Ile Asp Met Ser Gly Thr
290 295 300

Glu Pro Pro Gly Thr Glu Thr Thr Phe Asp Cys Gln Lys Met Ile Glu
305 310 315 320

Thr Pro Tyr Arg Ala Leu Gly Ser Asn Val Pro Arg Asp Asp Ser Ile
325 330 335

Arg Pro Gly Ala Thr Leu Pro Pro Phe Asp Thr Ala Ala Pro Asp Phe
340 345 350

Asp Thr Gly Thr Ser Pro Thr Pro Thr Thr Val Pro Glu Pro Ala Ile
355 360 365

Thr Thr Leu Ile Pro Arg Ser Thr Ser Asp Met Gly Phe Phe Ser Thr
 370 375 380
 Ala Arg Ala Thr Gly Ser Glu Thr Leu Ser Val Pro Val Gln Glu Thr
 385 390 395 400
 Asp Arg Thr Leu Ser Thr Thr Pro Leu Thr Leu Pro Leu Thr Pro Gly
 405 410 415
 Glu Ser Glu Asn Thr Leu Phe Pro Thr Thr Ala Pro Gly Ile Ser Thr
 420 425 430
 Glu Thr Pro Ser Ala Ala His Glu Thr Thr Gln Thr Gln Ser Ala Glu
 435 440 445
 Thr Val Val Phe Thr Gln Ser Pro Ser Thr Glu Ser Glu Thr Ala Arg
 450 455 460
 Ser Gln Ser Gln Glu Pro Trp Tyr Phe Thr Gln Thr Pro Ser Thr Glu
 465 470 475 480
 Gln Ala Ala Leu Thr Gln Thr Gln Ile Ala Glu Thr Glu Ala Leu Phe
 485 490 495
 Thr Gln Thr Pro Ser Ala Glu Gln Met Thr Phe Thr Gln Thr Pro Gly
 500 505 510
 Ala Glu Thr Glu Ala Pro Ala Gln Thr Pro Ser Thr Ile Pro Glu Ile
 515 520 525
 Phe Thr Gln Ser Arg Ser Thr Pro Pro Glu Thr Ala Arg Ala Pro Ser
 530 535 540
 Ala Ala Pro Glu Val Phe Thr Gln Ser Ser Ser Thr Val Thr Glu Val
 545 550 555 560
 Phe Thr Gln Thr Pro Ser Thr Val Pro Lys Thr Thr Leu Ser Ser Ser
 565 570 575
 Thr Glu Pro Ala Ile Phe Thr Arg Thr Gln Ser Ala Gly Thr Glu Ala
 580 585 590
 Phe Thr Gln Thr Ser Ser Ala Glu Pro Asp Thr Met Arg Thr Gln Ser
 595 600 605
 Thr Glu Thr His Phe Phe Thr Gln Ala Pro Ser Thr Val Pro Lys Ala
 610 615 620
 Thr Gln Thr Pro Ser Thr Glu Pro Glu Val Leu Thr Gln Ser Pro Ser
 625 630 635 640
 Thr Glu Pro Val Pro Phe Thr Arg Thr Leu Gly Ala Glu Pro Glu Ile
 645 650 655
 Thr Gln Thr Pro Ser Ala Ala Pro Glu Val Tyr Thr Arg Ser Ser Ser
 660 665 670
 Thr Met Pro Glu Thr Ala Gln Ser Thr Pro Leu Ala Ser Gln Asn Pro
 675 680 685
 Thr Ser Ser Gly Thr Gly Thr His Asn Thr Glu Pro Arg Thr Tyr Pro
 690 695 700
 Val Gln Thr Thr Pro His Thr Gln Lys Leu Tyr Thr Glu Asn Lys Thr
 705 710 715 720

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Leu Ser Phe Pro Thr Val Val Ser Glu Phe His Glu Met Ser Thr Ala
725 730 735

Glu Ser Gln Thr Pro Leu Leu Asp Val Lys Ile Val Glu Val Lys Phe
740 745 750

Ser Asn Asp Gly Glu Val Thr Ala Thr Cys Val Ser Thr Val Lys Ser
755 760 765

Pro Tyr Arg Val Glu Thr Asn Trp Lys Val Asp Leu Val Asp Val Met
770 775 780

Asp Glu Ile Ser Gly Asn Ser Pro Ala Gly Val Phe Asn Ser Asn Glu
785 790 795 800

Lys Trp Gln Lys Gln Leu Tyr Tyr Arg Val Thr Asp Gly Arg Thr Ser
805 810 815

Val Gln Leu Met Cys Leu Ser Cys Thr Ser His Ser Pro Glu Pro Tyr
820 825 830

Cys Leu Phe Asp Thr Ser Leu Ile Ala Arg Glu Lys Asp Ile Ala Pro
835 840 845

Glu Leu Tyr Phe Thr Ser Asp Pro Gln Thr Ala Tyr Cys Thr Ile Thr
850 855 860

Leu Pro Ser Gly Val Val Pro Arg Phe Glu Trp Ser Leu Asn Asn Val
865 870 875 880

Ser Leu Pro Glu Tyr Leu Thr Ala Thr Thr Val Val Ser His Thr Ala
885 890 895

Gly Gln Ser Thr Val Trp Lys Ser Ser Ala Arg Ala Gly Glu Ala Trp
900 905 910

Ile Ser Gly Arg Gly Gly Asn Ile Tyr Glu Cys Thr Val Leu Ile Ser
915 920 925

Asp Gly Thr Arg Val Thr Thr Arg Lys Glu Arg Cys Leu Thr Asn Thr
930 935 940

Trp Ile Ala Val Glu Asn Gly Ala Ala Gln Ala Gln Leu Tyr Ser Leu
945 950 955 960

Phe Ser Gly Leu Val Ser Gly Leu Cys Gly Ser Ile Ser Ala Leu Tyr
965 970 975

Ala Thr Leu Trp Thr Ala Ile Tyr Phe
980 985

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ala Ser Leu Leu Gly Thr Leu Ala Leu Leu Ala Ala Thr Leu Ala
1 5 10 15

Pro Phe Gly Ala Met Gly Ile Val Ile Thr Gly Asn His Val Ser Ala
20 25 30

Arg Ile Asp Asp Asp His Ile Val Ile Val Ala Pro Arg Pro Glu Ala
35 40 45

Thr Ile Gln Leu Gln Leu Phe Phe Met Pro Gly Gln Arg Pro His Lys
50 55 60

Pro Tyr Ser Gly Thr Val Arg Val Ala Phe Arg Ser Asp Ile Thr Asn
65 70 75 80

Gln Cys Tyr Gln Glu Leu Ser Glu Glu Arg Phe Glu Asn Cys Thr His
85 90 95

Arg Ser Ser Ser Val Phe Val Gly Cys Lys Val Thr Glu Tyr Thr Phe
100 105 110

Ser Ala Ser Asn Arg Leu Thr Gly Pro Pro His Pro Phe Lys Leu Thr
115 120 125

Ile Arg Asn Pro Arg Pro Asn Asp Ser Gly Met Phe Tyr Val Ile Val
130 135 140

Arg Leu Asp Asp Thr Lys Glu Pro Ile Asp Val Phe Ala Ile Gln Leu
145 150 155 160

Ser Val Tyr Gln Phe Ala Asn Thr Ala Ala Thr Arg Gly Leu Tyr Ser
165 170 175

Lys Ala Ser Cys Arg Thr Phe Gly Leu Pro Thr Val Gln Leu Glu Ala
180 185 190

Tyr Leu Arg Thr Glu Glu Ser Trp Arg Asn Trp Gln Ala Tyr Val Ala
195 200 205

Thr Glu Ala Thr Thr Thr Ser Ala Glu Ala Thr Thr Pro Thr Pro Val
210 215 220

Thr Ala Thr Ser Ala Ser Glu Leu Glu Ala Glu His Phe Thr Phe Pro
225 230 235 240

Trp Leu Glu Asn Gly Val Asp His Tyr Glu Pro Thr Pro Ala Asn Glu
245 250 255

Asn Ser Asn Val Thr Val Arg Leu Gly Thr Met Ser Pro Thr Leu Ile
260 265 270

Gly Val Thr Val Ala Ala Val Val Ser Ala Thr Ile Gly Leu Val Ile
275 280 285

Val Ile Ser Ile Val Thr Arg Asn Met Cys Thr Pro His Arg Lys Leu
290 295 300

Asp Thr Val Ser Gln Asp Asp Glu Glu Arg Ser Gln Thr Arg Arg Glu
305 310 315 320

Ser Arg Lys Phe Gly Pro Met Val Ala Cys Glu Ile Asn Lys Gly Ala
325 330 335

Asp Gln Asp Ser Glu Leu Val Glu Leu Val Ala Ile Val Asn Pro Ser
340 345 350

Ala Leu Ser Ser Pro Asp Ser Ile Lys Met
355 360

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 499 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Asn	Met	Leu	Val	Ile	Val	Leu	Ala	Ser	Cys	Leu	Ala	Arg	Leu	Thr	1	5	10	15
Phe	Ala	Thr	Arg	His	Val	Leu	Phe	Leu	Glu	Gly	Thr	Gln	Ala	Val	Leu	20	25	30	
Gly	Glu	Asp	Asp	Pro	Arg	Asn	Val	Pro	Glu	Gly	Thr	Val	Ile	Lys	Trp	35	40	45	
Thr	Lys	Val	Leu	Arg	Asn	Ala	Cys	Lys	Met	Lys	Ala	Ala	Asp	Val	Cys	50	55	60	
Ser	Ser	Pro	Asn	Tyr	Cys	Phe	His	Asp	Leu	Ile	Tyr	Asp	Gly	Gly	Lys	65	70	75	
Lys	Asp	Cys	Pro	Pro	Ala	Gly	Pro	Leu	Ser	Ala	Asn	Leu	Val	Ile	Leu	85	90	95	
Leu	Lys	Arg	Gly	Glu	Ser	Phe	Val	Val	Leu	Gly	Ser	Gly	Leu	His	Asn	100	105	110	
Ser	Asn	Ile	Thr	Asn	Ile	Met	Trp	Thr	Glu	Tyr	Gly	Gly	Leu	Leu	Phe	115	120	125	
Asp	Pro	Val	Thr	Arg	Ser	Asp	Glu	Gly	Ile	Tyr	Phe	Arg	Arg	Ile	Ser	130	135	140	
Gln	Pro	Asp	Leu	Ala	Met	Glu	Thr	Thr	Ser	Tyr	Asn	Val	Ser	Val	Leu	145	150	155	
Ser	His	Val	Asp	Glu	Lys	Ala	Pro	Ala	Pro	His	Glu	Val	Glu	Ile	Asp	165	170	175	
Thr	Ile	Lys	Pro	Ser	Glu	Ala	His	Ala	His	Val	Glu	Leu	Gln	Met	Leu	180	185	190	
Pro	Phe	His	Glu	Leu	Asn	Asp	Asn	Ser	Pro	Thr	Tyr	Val	Thr	Pro	Val	195	200	205	
Leu	Arg	Val	Phe	Pro	Pro	Thr	Glu	His	Val	Lys	Phe	Asn	Val	Thr	Tyr	210	215	220	
Ser	Trp	Tyr	Gly	Phe	Asp	Val	Lys	Glu	Glu	Cys	Glu	Glu	Val	Lys	Leu	225	230	235	
Phe	Glu	Pro	Cys	Val	Tyr	His	Pro	Thr	Asp	Gly	Lys	Cys	Gln	Phe	Pro	245	250	255	
Ala	Thr	Asn	Gln	Arg	Cys	Leu	Ile	Gly	Ser	Val	Leu	Met	Ala	Glu	Phe	260	265	270	
Leu	Gly	Ala	Ala	Ser	Leu	Leu	Asp	Cys	Ser	Arg	Asp	Thr	Leu	Glu	Asp	275	280	285	
Cys	His	Glu	Asn	Arg	Val	Pro	Asn	Leu	Arg	Phe	Asp	Ser	Arg	Leu	Ser	290	295	300	

Glu Ser Arg Ala Gly Leu Val Ile Ser Pro Leu Ile Ala Ile Pro Lys
 305 310 315 320
 Val Leu Ile Ile Val Val Ser Asp Gly Asp Ile Leu Gly Trp Ser Tyr
 325 330 335
 Thr Val Leu Gly Lys Arg Asn Ser Pro Arg Val Val Val Glu Thr His
 340 345 350
 Met Pro Ser Lys Val Pro Met Asn Lys Val Val Ile Gly Ser Pro Gly
 355 360 365
 Pro Met Asp Glu Thr Gly Asn Tyr Lys Met Tyr Phe Val Val Ala Gly
 370 375 380
 Val Ala Ala Thr Cys Val Ile Leu Thr Cys Ala Leu Leu Val Gly Lys
 385 390 395 400
 Lys Lys Cys Pro Ala His Gln Met Gly Thr Phe Ser Lys Thr Glu Pro
 405 410 415
 Leu Tyr Ala Pro Leu Pro Lys Asn Glu Phe Glu Ala Gly Gly Leu Thr
 420 425 430
 Asp Asp Glu Glu Val Ile Tyr Asp Glu Val Tyr Glu Pro Leu Phe Arg
 435 440 445
 Gly Tyr Cys Lys Gln Glu Phe Arg Glu Asp Val Asn Thr Phe Phe Gly
 450 455 460
 Ala Val Val Glu Gly Glu Arg Ala Leu Asn Phe Lys Ser Ala Ile Ala
 465 470 475 480
 Ser Met Ala Asp Arg Ile Leu Ala Asn Lys Ser Gly Arg Arg Asn Met
 485 490 495
 Asp Ser Tyr

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 260 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Pro Phe Lys Thr Arg Gly Ala Glu Asp Ala Ala Ala Gly Lys Asn
 1 5 10 15
 Arg Phe Lys Lys Ser Arg Asn Arg Glu Ile Leu Pro Thr Arg Leu Arg
 20 25 30
 Gly Thr Gly Lys Lys Thr Ala Gly Leu Ser Asn Tyr Thr Gln Pro Ile
 35 40 45
 Pro Trp Asn Pro Lys Phe Cys Ser Ala Arg Gly Glu Ser Asp Asn His
 50 55 60
 Ala Cys Lys Asp Thr Phe Tyr Arg Arg Thr Cys Cys Ala Ser Arg Ser
 65 70 75 80

Thr Val Ser Ser Gln Pro Asp Ser Pro His Thr Pro Met Pro Thr Glu
85 90 95

Tyr Gly Arg Val Pro Ser Ala Lys Arg Lys Lys Leu Ser Ser Ser Asp
100 105 110

Xaa Glu Gly Ala His Gln Pro Leu Val Ser Cys Lys Leu Pro Asp Ser
115 120 125

Gln Ala Ala Pro Ala Arg Thr Tyr Ser Ser Ala Gln Arg Tyr Thr Val
130 135 140

Asp Glu Val Ser Ser Pro Thr Pro Pro Gly Val Asp Ala Val Ala Asp
145 150 155 160

Leu Glu Thr Arg Ala Glu Leu Pro Gly Ala Thr Thr Glu Gln Thr Glu
165 170 175

Ser Lys Asn Lys Leu Pro Asn Gln Gln Ser Arg Leu Lys Pro Lys Pro
180 185 190

Thr Asn Glu His Val Gly Gly Glu Arg Cys Pro Ser Glu Gly Thr Val
195 200 205

Glu Ala Pro Ser Leu Gly Ile Leu Ser Arg Val Gly Ala Ala Ile Ala
210 215 220

Asn Glu Leu Ala Arg Met Arg Arg Ala Cys Leu Pro Leu Ala Ala Ser
225 230 235 240

Ala Ala Ala Ala Gly Ile Val Ala Trp Ala Ala Ala Arg Ala Leu Gln
245 250 255

Lys Gln Gly Arg
260

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1305 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..1305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATG CAC CGT CCT CAT CTC AGA CGG CAC TCG CGT TAC TAC GCG AAA GGA
Met His Arg Pro His Leu Arg Arg His Ser Arg Tyr Tyr Ala Lys Gly
1 5 10 15

GAG GTG CTT AAC AAA CAC ATG GAT TGC GGT GGA AAA CGG TGC TGC TCA
Glu Val Leu Asn Lys His Met Asp Cys Gly Gly Lys Arg Cys Cys Ser
20 25 30

48

96

GGC	GCA	GCT	GTA	TTC	ACT	CTT	TTC	TGG	ACT	TGT	GTC	AGG	ATT	ATG	CGG	144
Gly	Ala	Ala	Val	Phe	Thr	Leu	Phe	Trp	Thr	Cys	Val	Arg	Ile	Met	Arg	
		35					40					45				
GAG	CAT	ATC	TGC	TTT	GTA	CGC	AAC	GCT	ATG	GAC	CGC	CAT	TTA	TTT	TTG	192
Glu	His	Ile	Cys	Phe	Val	Arg	Asn	Ala	Met	Asp	Arg	His	Leu	Phe	Leu	
	50					55					60					
AGG	AAT	GCT	TTT	TGG	ACT	ATC	GTA	CTG	CTT	TCT	TCC	TTC	GCT	AGC	CAG	240
Arg	Asn	Ala	Phe	Trp	Thr	Ile	Val	Leu	Leu	Ser	Ser	Phe	Ala	Ser	Gln	
	65				70					75					80	
AGC	ACC	GCC	GCC	GTC	ACG	TAC	GAC	TAC	ATT	TTA	GGC	CGT	CGC	GCG	CTC	288
Ser	Thr	Ala	Ala	Val	Thr	Tyr	Asp	Tyr	Ile	Leu	Gly	Arg	Arg	Ala	Leu	
				85					90					95		
GAC	GCG	CTA	ACC	ATA	CCG	GCG	GTT	GGC	CCG	TAT	AAC	AGA	TAC	CTC	ACT	336
Asp	Ala	Leu		Ile	Pro	Ala	Val	Gly	Pro	Tyr	Asn	Arg	Tyr	Leu	Thr	
			100					105					110			
AGG	GTA	TCA	AGA	GGC	TGC	GAC	GTT	GTC	GAG	CTC	AAC	CCG	ATT	TCT	AAC	384
Arg	Val	Ser	Arg	Gly	Cys	Asp	Val	Val	Glu	Leu	Asn	Pro	Ile	Ser	Asn	
		115					120					125				
GTG	GAC	GAC	ATG	ATA	TCG	GCG	GCC	AAA	GAA	AAA	GAG	AAG	GGG	GGC	CCT	432
Val	Asp	Asp	Met	Ile	Ser	Ala	Ala	Lys	Glu	Lys	Glu	Lys	Gly	Gly	Pro	
	130					135					140					
TTC	GAG	GCC	TCC	GTC	GTC	TGG	TTC	TAC	GTG	ATT	AAG	GGC	GAC	GAC	GGC	480
Phe	Glu	Ala	Ser	Val	Val	Trp	Phe	Tyr	Val	Ile	Lys	Gly	Asp	Asp	Gly	
	145				150				155						160	
GAG	GAC	AAG	TAC	TGT	CCA	ATC	TAT	AGA	AAA	GAG	TAC	AGG	GAA	TGT	GGC	528
Glu	Asp	Lys	Tyr	Cys	Pro	Ile	Tyr	Arg	Lys	Glu	Tyr	Arg	Glu	Cys	Gly	
				165					170					175		
GAC	GTA	CAA	CTG	CTA	TCT	GAA	TGC	GCC	GTT	CAA	TCT	GCA	CAG	ATG	TGG	576
Asp	Val	Gln	Leu	Leu	Ser	Glu	Cys	Ala	Val	Gln	Ser	Ala	Gln	Met	Trp	
			180				185						190			
GCA	GTG	GAC	TAT	GTT	CCT	AGC	ACC	CTT	GTA	TCG	CGA	AAT	GGC	GCG	GGA	624
Ala	Val	Asp	Tyr	Val	Pro	Ser	Thr	Leu	Val	Ser	Arg	Asn	Gly	Ala	Gly	
		195					200					205				
CTG	ACT	ATA	TTC	TCC	CCC	ACT	GCT	GCG	CTC	TCT	GGC	CAA	TAC	TTG	CTG	672
Leu	Thr	Ile	Phe	Ser	Pro	Thr	Ala	Ala	Leu	Ser	Gly	Gln	Tyr	Leu	Leu	
	210					215					220					
ACC	CTG	AAA	ATC	GGG	AGA	TTT	GCG	CAA	ACA	GCT	CTC	GTA	ACT	CTA	GAA	720
Thr	Leu	Lys	Ile	Gly	Arg	Phe	Ala	Gln	Thr	Ala	Leu	Val	Thr	Leu	Glu	
	225				230					235					240	
GTT	AAC	GAT	CGC	TGT	TTA	AAG	ATC	GGG	TCG	CAG	CTT	AAC	TTT	TTA	CCG	768
Val	Asn	Asp	Arg	Cys	Leu	Lys	Ile	Gly	Ser	Gln	Leu	Asn	Phe	Leu	Pro	
				245				250						255		
TCG	AAA	TGC	TGG	ACA	ACA	GAA	CAG	TAT	CAG	ACT	GGA	TTT	CAA	GGC	GAA	816
Ser	Lys	Cys	Trp	Thr	Thr	Glu	Gln	Tyr	Gln	Thr	Gly	Phe	Gln	Gly	Glu	
			260				265						270			
CAC	CTT	TAT	CCG	ATC	GCA	GAC	ACC	AAT	ACA	CGA	CAC	GCG	GAC	GAC	GTA	864
His	Leu	Tyr	Pro	Ile	Ala	Asp	Thr	Asn	Thr	Arg	His	Ala	Asp	Asp	Val	
		275					280					285				
TAT	CGG	GGA	TAC	GAA	GAT	ATT	CTG	CAG	CGC	TGG	AAT	AAT	TTG	CTG	AGG	912
Tyr	Arg	Gly	Tyr	Glu	Asp	Ile	Leu	Gln	Arg	Trp	Asn	Asn	Leu	Leu	Arg	
	290					295					300					

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AAA AAG AAT CCT AGC GCG CCA GAC CCT CGT CCA GAT AGC GTC CCG CAA	960
Lys Lys Asn Pro Ser Ala Pro Asp Pro Arg Pro Asp Ser Val Pro Gln	
305 310 315 320	
GAA ATT CCC GCT GTA ACC AAG AAA GCG GAA GGG CGC ACC CCG GAC GCA	1008
Glu Ile Pro Ala Val Thr Lys Lys Ala Glu Gly Arg Thr Pro Asp Ala	
325 330 335	
GAA AGC AGC GAA AAG AAG GCC CCT CCA GAA GAC TCG GAG GAC GAC ATG	1056
Glu Ser Ser Glu Lys Lys Ala Pro Pro Glu Asp Ser Glu Asp Asp Met	
340 345 350	
CAG GCA GAG GCT TCT GGA GAA AAT CCT GCC GCC CTC CCC GAA GAC GAC	1104
Gln Ala Glu Ala Ser Gly Glu Asn Pro Ala Ala Leu Pro Glu Asp Asp	
355 360 365	
GAA GTC CCC GAG GAC ACC GAG CAC GAT GAT CCA AAC TCG GAT CCT GAC	1152
Glu Val Pro Glu Asp Thr Glu His Asp Asp Pro Asn Ser Asp Pro Asp	
370 375 380	
TAT TAC AAT GAC ATG CCC GCC GTG ATC CCG GTG GAG GAG ACT ACT AAA	1200
Tyr Tyr Asn Asp Met Pro Ala Val Ile Pro Val Glu Glu Thr Thr Lys	
385 390 395 400	
AGT TCT AAT GCC GTC TCC ATG CCC ATA TTC GCG GCG TTC GTA GCC TGC	1248
Ser Ser Asn Ala Val Ser Met Pro Ile Phe Ala Ala Phe Val Ala Cys	
405 410 415	
GCG GTC GCG CTC GTG GGG CTA CTG GTT TGG AGC ATC GTA AAA TGC GCG	1296
Ala Val Ala Leu Val Gly Leu Leu Val Trp Ser Ile Val Lys Cys Ala	
420 425 430	
CGT AGC TAA	1305
Arg Ser	
435	

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 434 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met His Arg Pro His Leu Arg Arg His Ser Arg Tyr Tyr Ala Lys Gly	
1 5 10 15	
Glu Val Leu Asn Lys His Met Asp Cys Gly Gly Lys Arg Cys Cys Ser	
20 25 30	
Gly Ala Ala Val Phe Thr Leu Phe Trp Thr Cys Val Arg Ile Met Arg	
35 40 45	
Glu His Ile Cys Phe Val Arg Asn Ala Met Asp Arg His Leu Phe Leu	
50 55 60	
Arg Asn Ala Phe Trp Thr Ile Val Leu Leu Ser Ser Phe Ala Ser Gln	
65 70 75 80	
Ser Thr Ala Ala Val Thr Tyr Asp Tyr Ile Leu Gly Arg Arg Ala Leu	
85 90 95	

Asp Ala Leu Thr Ile Pro Ala Val Gly Pro Tyr Asn Arg Tyr Leu Thr
 100 105 110
 Arg Val Ser Arg Gly Cys Asp Val Val Glu Leu Asn Pro Ile Ser Asn
 115 120 125
 Val Asp Asp Met Ile Ser Ala Ala Lys Glu Lys Glu Lys Gly Gly Pro
 130 135 140
 Phe Glu Ala Ser Val Val Trp Phe Tyr Val Ile Lys Gly Asp Asp Gly
 145 150 155 160
 Glu Asp Lys Tyr Cys Pro Ile Tyr Arg Lys Glu Tyr Arg Glu Cys Gly
 165 170 175
 Asp Val Gln Leu Leu Ser Glu Cys Ala Val Gln Ser Ala Gln Met Trp
 180 185 190
 Ala Val Asp Tyr Val Pro Ser Thr Leu Val Ser Arg Asn Gly Ala Gly
 195 200 205
 Leu Thr Ile Phe Ser Pro Thr Ala Ala Leu Ser Gly Gln Tyr Leu Leu
 210 215 220
 Thr Leu Lys Ile Gly Arg Phe Ala Gln Thr Ala Leu Val Thr Leu Glu
 225 230 235 240
 Val Asn Asp Arg Cys Leu Lys Ile Gly Ser Gln Leu Asn Phe Leu Pro
 245 250 255
 Ser Lys Cys Trp Thr Thr Glu Gln Tyr Gln Thr Gly Phe Gln Gly Glu
 260 265 270
 His Leu Tyr Pro Ile Ala Asp Thr Asn Thr Arg His Ala Asp Asp Val
 275 280 285
 Tyr Arg Gly Tyr Glu Asp Ile Leu Gln Arg Trp Asn Asn Leu Leu Arg
 290 295 300
 Lys Lys Asn Pro Ser Ala Pro Asp Pro Arg Pro Asp Ser Val Pro Gln
 305 310 315 320
 Glu Ile Pro Ala Val Thr Lys Lys Ala Glu Gly Arg Thr Pro Asp Ala
 325 330 335
 Glu Ser Ser Glu Lys Lys Ala Pro Pro Glu Asp Ser Glu Asp Asp Met
 340 345 350
 Gln Ala Glu Ala Ser Gly Glu Asn Pro Ala Ala Leu Pro Glu Asp Asp
 355 360 365
 Glu Val Pro Glu Asp Thr Glu His Asp Asp Pro Asn Ser Asp Pro Asp
 370 375 380
 Tyr Tyr Asn Asp Met Pro Ala Val Ile Pro Val Glu Glu Thr Thr Lys
 385 390 395 400
 Ser Ser Asn Ala Val Ser Met Pro Ile Phe Ala Ala Phe Val Ala Cys
 405 410 415
 Ala Val Ala Leu Val Gly Leu Leu Val Trp Ser Ile Val Lys Cys Ala
 420 425 430
 Arg Ser

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 690 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATG GCG CCT GTA AAA GTG ACT ATA GTT TCT GCG GTC GAT TCG CAC TAC	48
Met Ala Pro Val Lys Val Thr Ile Val Ser Ala Val Asp Ser His Tyr	
1 5 10 15	
AAA CTA CCT AAT TCT AGA TTT GAG CTC TCG GAT TCT GGA TGG AAA GAA	96
Lys Leu Pro Asn Ser Arg Phe Glu Leu Ser Asp Ser Gly Trp Lys Glu	
20 25 30	
TTG GTT CAC GCA GTG AAA ACT ATG GCG AGT TAC GAT CGT CCG AGT ACA	144
Leu Val His Ala Val Lys Thr Met Ala Ser Tyr Asp Arg Pro Ser Thr	
35 40 45	
TTA TCG GTA ATC GTG CGC CCG GCA TCT CTG TAC GAA GTT TCC GGG GAG	192
Leu Ser Val Ile Val Arg Pro Ala Ser Leu Tyr Glu Val Ser Gly Glu	
50 55 60	
CTG TTT TCC CTT CCC AGG ATG TGC AGA CCC GTG ATT CGG TTC GGT GAG	240
Leu Phe Ser Leu Pro Arg Met Cys Arg Pro Val Ile Arg Phe Gly Glu	
65 70 75 80	
GGG GGC GAC CCG CCT GGA GTA AGT CCC GAG TGG AGC GGC TTG GAC GCA	288
Gly Gly Asp Pro Pro Gly Val Ser Pro Glu Trp Ser Gly Leu Asp Ala	
85 90 95	
GGG TTT TAC CAT TTG TCA TCT GGC GCG TAT GCC GCA AAA GAG TTC CAT	336
Gly Phe Tyr His Leu Ser Ser Gly Ala Tyr Ala Ala Lys Glu Phe His	
100 105 110	
TTG TGG GTG CTG GGT ACC GCT GAC ATA TGC ATG GCA GCT TTA AAC CTC	384
Leu Trp Val Leu Gly Thr Ala Asp Ile Cys Met Ala Ala Leu Asn Leu	
115 120 125	
CCT GCG CCA AAA ACT TTC CTA ATT ACC GAA ACC GGA GGT AAA AAT TTT	432
Pro Ala Pro Lys Thr Phe Leu Ile Thr Glu Thr Gly Gly Lys Asn Phe	
130 135 140	
GAG AGA GGA GTG GAA ATA TTT TTG GTA AAC GGA GAC AAG ACA ACG CTG	480
Glu Arg Gly Val Glu Ile Phe Leu Val Asn Gly Asp Lys Thr Thr Leu	
145 150 155 160	
TCT CTG AGT CAC CCA TCA GTC TGG ACA ACT CTT GCC CCT TCG AGC CTG	528
Ser Leu Ser His Pro Ser Val Trp Thr Thr Leu Ala Pro Ser Ser Leu	
165 170 175	

AGA	ACG	CCC	TGG	CCG	TAC	AGC	ACG	GTA	AAG	TTT	TTA	AAA	GTA	AAA	CCT	576
Arg	Thr	Pro	Trp	Pro	Tyr	Ser	Thr	Val	Lys	Phe	Leu	Lys	Val	Lys	Pro	
			180					185					190			
AAC	TCG	GCC	GCA	TAC	TGT	GTT	TCC	GAC	TCG	GAT	GAT	GGC	GAA	CGG	CAG	624
Asn	Ser	Ala	Ala	Tyr	Cys	Val	Ser	Asp	Ser	Asp	Asp	Gly	Glu	Arg	Gln	
		195					200					205				
CCA	AAA	TTT	TTT	CTC	GGG	AGT	CTA	TTT	AAG	TCG	AAG	AAA	CCC	CGC	TCC	672
Pro	Lys	Phe	Phe	Leu	Gly	Ser	Leu	Phe	Lys	Ser	Lys	Lys	Pro	Arg	Ser	
	210					215					220					
CCG	CGG	CGC	CGA	CGT	TA	G										690
Pro	Arg	Arg	Arg	Arg												
225																

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Ala	Pro	Val	Lys	Val	Thr	Ile	Val	Ser	Ala	Val	Asp	Ser	His	Tyr	
1				5					10					15		
Lys	Leu	Pro	Asn	Ser	Arg	Phe	Glu	Leu	Ser	Asp	Ser	Gly	Trp	Lys	Glu	
			20					25					30			
Leu	Val	His	Ala	Val	Lys	Thr	Met	Ala	Ser	Tyr	Asp	Arg	Pro	Ser	Thr	
		35					40					45				
Leu	Ser	Val	Ile	Val	Arg	Pro	Ala	Ser	Leu	Tyr	Glu	Val	Ser	Gly	Glu	
	50					55					60					
Leu	Phe	Ser	Leu	Pro	Arg	Met	Cys	Arg	Pro	Val	Ile	Arg	Phe	Gly	Glu	
	65				70					75					80	
Gly	Gly	Asp	Pro	Pro	Gly	Val	Ser	Pro	Glu	Trp	Ser	Gly	Leu	Asp	Ala	
				85					90					95		
Gly	Phe	Tyr	His	Leu	Ser	Ser	Gly	Ala	Tyr	Ala	Ala	Lys	Glu	Phe	His	
			100					105					110			
Leu	Trp	Val	Leu	Gly	Thr	Ala	Asp	Ile	Cys	Met	Ala	Ala	Leu	Asn	Leu	
		115					120					125				
Pro	Ala	Pro	Lys	Thr	Phe	Leu	Ile	Thr	Glu	Thr	Gly	Gly	Lys	Asn	Phe	
	130					135					140					
Glu	Arg	Gly	Val	Glu	Ile	Phe	Leu	Val	Asn	Gly	Asp	Lys	Thr	Thr	Leu	
	145				150					155					160	
Ser	Leu	Ser	His	Pro	Ser	Val	Trp	Thr	Thr	Leu	Ala	Pro	Ser	Ser	Leu	
			165					170						175		
Arg	Thr	Pro	Trp	Pro	Tyr	Ser	Thr	Val	Lys	Phe	Leu	Lys	Val	Lys	Pro	
			180					185					190			
Asn	Ser	Ala	Ala	Tyr	Cys	Val	Ser	Asp	Ser	Asp	Asp	Gly	Glu	Arg	Gln	
		195					200					205				

Pro Lys Phe Phe Leu Gly Ser Leu Phe Lys Ser Lys Lys Pro Arg Ser
210 215 220

Pro Arg Arg Arg Arg
225

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 381 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATG CGT AGC TCA GTT ACG TCA TTG TGG AGC CCT TCA GAT CAC GCC TCT	48
Met Arg Ser Ser Val Thr Ser Leu Trp Ser Pro Ser Asp His Ala Ser	
1 5 10 15	
TCG CCC GCA AAT GCC AAG CAT TTT TAT CAT ATT TCC GAT TTC CGG CGC	96
Ser Pro Ala Asn Ala Lys His Phe Tyr His Ile Ser Asp Phe Arg Arg	
20 25 30	
GCG GAA ACG GCG CCT GCG GGC GGT ACG GGC GCG CGA ACT GAG GTT AAG	144
Ala Glu Thr Ala Pro Ala Gly Thr Gly Ala Arg Thr Glu Val Lys	
35 40 45	
CGT CGC GCT TTC ACT TTC CCA GCG GCA GCG GTA CTC AGC GCA ACT GAA	192
Arg Arg Ala Phe Thr Phe Pro Ala Ala Ala Val Leu Ser Ala Thr Glu	
50 55 60	
GCC CGA ACC GGC TCG TCT ATC ACC GGC TTA AAC CGT ACT CCG TCT GCA	240
Ala Arg Thr Gly Ser Ser Ile Thr Gly Leu Asn Arg Thr Pro Ser Ala	
65 70 75 80	
ATA ATT TCC CTT GCA TGG TCC GAA ATG AGA AAT CTT AAG GAC CCC CTC	288
Ile Ile Ser Leu Ala Trp Ser Glu Met Arg Asn Leu Lys Asp Pro Leu	
85 90 95	
GGG TCC CTG TCG CTG GAA ATA GCT TTA ACG AAT GTC TCT AAC TTT TCC	336
Gly Ser Leu Ser Leu Glu Ile Ala Leu Thr Asn Val Ser Asn Phe Ser	
100 105 110	
CTC TTG AGC TCA GAC CCC ATG GCC TTC GAA AAG TCT TCA TAT TG	380
Leu Leu Ser Ser Asp Pro Met Ala Phe Glu Lys Ser Ser Tyr	
115 120 125	
A	381

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```

Met Arg Ser Ser Val Thr Ser Leu Trp Ser Pro Ser Asp His Ala Ser
 1           5           10           15
Ser Pro Ala Asn Ala Lys His Phe Tyr His Ile Ser Asp Phe Arg Arg
          20           25           30
Ala Glu Thr Ala Pro Ala Gly Gly Thr Gly Ala Arg Thr Glu Val Lys
          35           40           45
Arg Arg Ala Phe Thr Phe Pro Ala Ala Ala Val Leu Ser Ala Thr Glu
          50           55           60
Ala Arg Thr Gly Ser Ser Ile Thr Gly Leu Asn Arg Thr Pro Ser Ala
          65           70           75           80
Ile Ile Ser Leu Ala Trp Ser Glu Met Arg Asn Leu Lys Asp Pro Leu
          85           90           95
Gly Ser Leu Ser Leu Glu Ile Ala Leu Thr Asn Val Ser Asn Phe Ser
          100          105          110
Leu Leu Ser Ser Asp Pro Met Ala Phe Glu Lys Ser Ser Tyr
          115          120          125

```

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 879 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..878

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```

ATG TGG TGT CGT TTG CAC TGG ATA AGT CCT CGG TTC AGT ATT ATG CGT      48
Met Trp Cys Arg Leu His Trp Ile Ser Pro Arg Phe Ser Ile Met Arg
 1           5           10           15
CCC GGT TCC CGA ACT GGT AGG GTT TTG CGA GGC CAG GGG TGT GCT CTG      96
Pro Gly Ser Arg Thr Gly Arg Val Leu Arg Gly Gln Gly Cys Ala Leu
          20           25           30
TGC AGT TTC TGG CAT CGT ACT CGA ACT CCG AGT ATA AAC CTC CGG TGC      144
Cys Ser Phe Trp His Arg Thr Arg Thr Pro Ser Ile Asn Leu Arg Cys
          35           40           45

```

CGC GCT CGG GGT CTG AGT AAT TTC CGG CTC TGC GCC CAG AGT CCG GGT Arg Ala Arg Gly Leu Ser Asn Phe Arg Leu Cys Ala Gln Ser Pro Gly 50 55 60	192
GAA AGG CAC AGG TTC GGT ACT CGG ACT CTG AGT CAA CAC CTC CGG CTC Glu Arg His Arg Phe Gly Thr Arg Thr Leu Ser Gln His Leu Arg Leu 65 70 75 80	240
TGT ACT CGG AGT CTG AGT AGC TTT CGG TAC CGT ACT CGG GGC CTG AGT Cys Thr Arg Ser Leu Ser Ser Phe Arg Tyr Arg Thr Arg Gly Leu Ser 85 90 95	288
GAA AAA GTG TGT TTC AGT ACT CTG AGT TCG CAT AGT GTC CGG CTC GGC Glu Lys Val Cys Phe Ser Thr Leu Ser Ser His Ser Val Arg Leu Gly 100 105 110	336
ACT CGA AGT CTG AGT AAA GGC CTC AGT TCC CGC GCT CTG AGT CCG AGT Thr Arg Ser Leu Ser Lys Gly Leu Ser Ser Arg Ala Leu Ser Pro Ser 115 120 125	384
AAA AAT CGC CGG TTC AGT ACT CGA ACT CAG AGT AGT TTT CGG TAC CGT Lys Asn Arg Arg Phe Ser Thr Arg Thr Gln Ser Ser Phe Arg Tyr Arg 130 135 140	432
GCT CGG GGT CTG AGT AAA CAC CTC CGT TAC CGT ACT CGA ACT CTG TGT Ala Arg Gly Leu Ser Lys His Leu Arg Tyr Arg Thr Arg Thr Leu Cys 145 150 155 160	480
AAA AAC CTC CGG CGC CGC GCT CGG AGC GCG AGC GGT TTC GGG GGG CGT Lys Asn Leu Arg Arg Arg Ala Arg Ser Ala Ser Gly Phe Gly Gly Arg 165 170 175	528
GCT ACG AGA CTG AGT AAA TAT CTC GGG TAT CGT GCT CGG GGT CTG GGC Ala Thr Arg Leu Ser Lys Tyr Leu Gly Tyr Arg Ala Arg Gly Leu Gly 180 185 190	576
AGG TGC CTC GGT TTC TGC ACC CGG AGT CTG AGT AAA AGT CAT CTG TTC Arg Cys Leu Gly Phe Cys Thr Arg Ser Leu Ser Lys Ser His Leu Phe 195 200 205	624
AGC ACT CGG AGT CTG AGT AAA CAA CGC CTC CGT TTC TGC GAT CTG CGT Ser Thr Arg Ser Leu Ser Lys Gln Arg Leu Arg Phe Cys Asp Leu Arg 210 215 220	672
CTG AGT AAG AGC CGC CTG TTC AGT ACT CGG AGT CTG AGT AAA ATA CCA Leu Ser Lys Ser Arg Leu Phe Ser Thr Arg Ser Leu Ser Lys Ile Pro 225 230 235 240	720
CGG TTC CTG ACT CTG GGA CCG CGC GGT TTC CGA CTC GGT ACT CGG ACT Arg Phe Leu Thr Leu Gly Pro Arg Gly Phe Arg Leu Gly Thr Arg Thr 245 250 255	768
CTG AGT AAA GAC CAC CGT TTC TGC ACT CTG GGT CTG TGT AGT TTC ATG Leu Ser Lys Asp His Arg Phe Cys Thr Leu Gly Leu Cys Ser Phe Met 260 265 270	816
TGC CGC GCT CGG GGT CTC GGT AGA AAT CCC CGG CGC GGT CGT AGG AAA Cys Arg Ala Arg Gly Leu Gly Arg Asn Pro Arg Arg Gly Arg Arg Lys 275 280 285	864
CAG TGT ATT TTC TG A Gln Cys Ile Phe 290	879

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 292 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Trp Cys Arg Leu His Trp Ile Ser Pro Arg Phe Ser Ile Met Arg
 1 5 10 15
 Pro Gly Ser Arg Thr Gly Arg Val Leu Arg Gly Gln Gly Cys Ala Leu
 20 25 30
 Cys Ser Phe Trp His Arg Thr Arg Thr Pro Ser Ile Asn Leu Arg Cys
 35 40 45
 Arg Ala Arg Gly Leu Ser Asn Phe Arg Leu Cys Ala Gln Ser Pro Gly
 50 55 60
 Glu Arg His Arg Phe Gly Thr Arg Thr Leu Ser Gln His Leu Arg Leu
 65 70 75 80
 Cys Thr Arg Ser Leu Ser Ser Phe Arg Tyr Arg Thr Arg Gly Leu Ser
 85 90 95
 Glu Lys Val Cys Phe Ser Thr Leu Ser Ser His Ser Val Arg Leu Gly
 100 105 110
 Thr Arg Ser Leu Ser Lys Gly Leu Ser Ser Arg Ala Leu Ser Pro Ser
 115 120 125
 Lys Asn Arg Arg Phe Ser Thr Arg Thr Gln Ser Ser Phe Arg Tyr Arg
 130 135 140
 Ala Arg Gly Leu Ser Lys His Leu Arg Tyr Arg Thr Arg Thr Leu Cys
 145 150 155 160
 Lys Asn Leu Arg Arg Arg Ala Arg Ser Ala Ser Gly Phe Gly Gly Arg
 165 170 175
 Ala Thr Arg Leu Ser Lys Tyr Leu Gly Tyr Arg Ala Arg Gly Leu Gly
 180 185 190
 Arg Cys Leu Gly Phe Cys Thr Arg Ser Leu Ser Lys Ser His Leu Phe
 195 200 205
 Ser Thr Arg Ser Leu Ser Lys Gln Arg Leu Arg Phe Cys Asp Leu Arg
 210 215 220
 Leu Ser Lys Ser Arg Leu Phe Ser Thr Arg Ser Leu Ser Lys Ile Pro
 225 230 235 240
 Arg Phe Leu Thr Leu Gly Pro Arg Gly Phe Arg Leu Gly Thr Arg Thr
 245 250 255
 Leu Ser Lys Asp His Arg Phe Cys Thr Leu Gly Leu Cys Ser Phe Met
 260 265 270
 Cys Arg Ala Arg Gly Leu Gly Arg Asn Pro Arg Arg Gly Arg Arg Lys
 275 280 285
 Gln Cys Ile Phe
 290

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 534 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..533

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATG CTC CCA AGC CTA CTC AAC AGG GGC TCT CCC CGG CTG AAT TCT CCT	48
Met Leu Pro Ser Leu Leu Asn Arg Gly Ser Pro Arg Leu Asn Ser Pro	
1 5 10 15	
CCT AAG TGT TCA GAG GCC TCT GCT GTA CCA TAT AAC TAT CGT GTA GTA	96
Pro Lys Cys Ser Glu Ala Ser Ala Val Pro Tyr Asn Tyr Arg Val Val	
20 25 30	
CGC CCC TCC CAG TCC GTG TCC GAT ACT GCC CCT TTT GAG AGG ATT GGG	144
Arg Pro Ser Gln Ser Val Ser Asp Thr Ala Pro Phe Glu Arg Ile Gly	
35 40 45	
AGA TTA GAG AAT CGA AAT GAT TGG AGA GCC ACA TTC AGA CTT AAT CAC	192
Arg Leu Glu Asn Arg Asn Asp Trp Arg Ala Thr Phe Arg Leu Asn His	
50 55 60	
ATT TTT ATT GAG TCG GGC GAG CTT AGC GCA GAC GGG TTA ACA ATC GCA	240
Ile Phe Ile Glu Ser Gly Glu Leu Ser Ala Asp Gly Leu Thr Ile Ala	
65 70 75 80	
ACC AGT TCC ACA AGT TCA CTA TCC TGG TCA GCG CCC TTG TTT ATT TCG	288
Thr Ser Ser Thr Ser Ser Leu Ser Trp Ser Ala Pro Leu Phe Ile Ser	
85 90 95	
CAC GCA ACC ATG GGT CCA AAT TTT CGC GAT TCC CTT CTA GTT TGG GAA	336
His Ala Thr Met Gly Pro Asn Phe Arg Asp Ser Leu Leu Val Trp Glu	
100 105 110	
CGT TCT TCG TCG TCT TGC GAG ACC GTG TCT AAT TTT CGG TGC GGG GTG	384
Arg Ser Ser Ser Ser Cys Glu Thr Val Ser Asn Phe Arg Cys Gly Val	
115 120 125	
CAC ATG TTT CTG GTG ACG ATG GAA ATT ACA ATG ACG AGG CCG ATC GTT	432
His Met Phe Leu Val Thr Met Glu Ile Thr Met Thr Arg Pro Ile Val	
130 135 140	
GCG CTC ACG ACG GCA GCC ACG GTT ACC CCA ATT AGC GTA GGG CTC ATT	480
Ala Leu Thr Thr Ala Ala Thr Val Thr Pro Ile Ser Val Gly Leu Ile	
145 150 155 160	
GTC CCG AGA CGG ACA GTA ACG TTT GAA TTT TCG TTT GCG GGT GTC GGT	528
Val Pro Arg Arg Thr Val Thr Phe Glu Phe Ser Phe Ala Gly Val Gly	
165 170 175	
TCG TA A	534
Ser	

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 177 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```

Met Leu Pro Ser Leu Leu Asn Arg Gly Ser Pro Arg Leu Asn Ser Pro
 1           5           10           15
Pro Lys Cys Ser Glu Ala Ser Ala Val Pro Tyr Asn Tyr Arg Val Val
          20           25           30
Arg Pro Ser Gln Ser Val Ser Asp Thr Ala Pro Phe Glu Arg Ile Gly
          35           40           45
Arg Leu Glu Asn Arg Asn Asp Trp Arg Ala Thr Phe Arg Leu Asn His
          50           55           60
Ile Phe Ile Glu Ser Gly Glu Leu Ser Ala Asp Gly Leu Thr Ile Ala
          65           70           75           80
Thr Ser Ser Thr Ser Ser Leu Ser Trp Ser Ala Pro Leu Phe Ile Ser
          85           90           95
His Ala Thr Met Gly Pro Asn Phe Arg Asp Ser Leu Leu Val Trp Glu
          100          105          110
Arg Ser Ser Ser Ser Cys Glu Thr Val Ser Asn Phe Arg Cys Gly Val
          115          120          125
His Met Phe Leu Val Thr Met Glu Ile Thr Met Thr Arg Pro Ile Val
          130          135          140
Ala Leu Thr Thr Ala Ala Thr Val Thr Pro Ile Ser Val Gly Leu Ile
          145          150          155          160
Val Pro Arg Arg Thr Val Thr Phe Glu Phe Ser Phe Ala Gly Val Gly
          165          170          175
Ser
  
```

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 48 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GAATTCGAGC TCGGTACCCG GATAATACGT ACATGTTAAC GCAGAGGT

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GCTGACCGCT AGTCGACCTG CAGTGAATAA TAAAAAT

36

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TGTCCGTCGA GATCCTCTAG AGTCGACGAA AGGTCAGAGA CGATGCCC

48

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CGGATCAGAA ACTCTTTCGG TACCCGGGAT CCTCTAGA

38

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GAATACAAGC TTAGATGCAT ATTTACTCGA GCC

33

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GGTTTGGCGG AGCGGATATG ATCTCGACCT GCAGTGAATA ATAAATGTG T

51

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TGTCCGTCGA GATCCTCTAG AGTCGAGATC AGCAAATGT TCACGGGG

48

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

AAGCTTGGCG TAATCATG

18

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GGAATTCGAG CTCGGTACCT CGTGGCGAGC GCAGGCGGC

39

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGCCGAGTTA GGTTTTACTT TTCTAGAGGA TCCCCTCGAC GTCTGGGGCG C

51

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TTGCTGCGTT CCCGGGGATC CTCTAGAATT AGGTAGTTTG TAGTGCGA

48

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TCAAGATCCA GGAAATCCTT CGGTACCGAG CTCGAATTCTG TA

42

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GAATTCGAGC TCGGTACCGA AAGCTACTCA GAC

33

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CGCAAACAGC TCTCGTAACT CTAGAAGTTA ACGATCGCTG TT

42

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GAATAGCATA CCAATGCCTA TTCATTGGGA CTCGACTCTA GAGGATCCCC GGAACG

57

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TCGAGGGGAT CCTCTAGAGT CGAGGGACCC ATGGTTGCGT GC

42

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TTTACTAAAG CGCGGCGAAA GCTTCGTCGT GCTGGGTTCT GG

42

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

AAGCTTGGCG TAATCATGGT C

21

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GGAATTCGAG CTCGGTACCC GGATAATACG TACATGTAA CGCAGAGG

48

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

ATCTATTGGA GCGTTTAGCG CGCGTCGACG AAAGGTCAGA GACGA

45

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CTGCTTCATT TCTGATCCCC GGAACG

27

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ACCACCCCCG CGCCCCAGAC GTCGAGGGGA TCAATTATTG CGTATTGAAT A

51

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ATCAGAACT CTTTCGGTAC CGAGCTCGAA TTC

33

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GAATTCGAGC TCGGTACCCG GATAATACGT ACATGTTAAC GCAGAGGT

48

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GCTGACCGCT AGTCGACTCT AGAGGATCCC CTC

33

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CGTTCCCGGG GATCCTCTAG AGTCGACGGC AGAGTCGCAG AC

42

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TGATCCAAAC TCGGATCCTC TAGAGTCGAC

30

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

AAGCTTGGGC TGCAGGTCGA CTCTAGAGGA TCCCCTCGAC GTCTGGGG

48

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CACACCTTTG CGCATCTCCA CAGCTCAACA ATGAATTCCA TGTTACGTCC TGTAGAAACC

60

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CAGGGAGGCA AACAAATGAAT CAACAACTCT CCCGGGAGAT GGGGGAGGCT AACTGAAACA

60

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

TGCTGCGTTC CCGGGGATCC TCTAGAGTCG ACCTGCAGCC CAAGC

45

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TCTAGAGTCG ACCTGCAGTG AATAATAAAA TGTGTGTTTG TCCGAAAT

48

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CTCCATAGAA GACACCGGGA CCATGGATCC CGTCGTTTTA CAACG

45

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TCGGCGGAAA TCCAGCTGAG CGCCGGTCGC TACCATTACC AGTTGGTCTG GTGTCAAAAA
GATCTAGAAT AAGCTAGAGG ATCGATCCCC TATGGCGATC ATCAG

60

105

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CCGTCGAGAT CCTCTAGAGT CGACCTGCAG GTCGAC

36

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: N
- (iv) ANTI-SENSE: N

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CCTAGCACCC TTGTATCGCG

20

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: N
- (iv) ANTI-SENSE: N

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CGCCTCGAGT CCAATGAAT AGGCATTGG

29

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: N
- (iv) ANTI-SENSE: N

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CGCCTCGAGG ACCCATGGTT GCGTGCG

27

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CTCGTCCGAA CGAGTTACAG

20

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18912 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 697..1533
- (D) OTHER INFORMATION:

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: complement (1900..2784)
- (D) OTHER INFORMATION:

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: complement (2916..3605)
- (D) OTHER INFORMATION:

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3694..5124
- (D) OTHER INFORMATION:

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 5210..7081
- (D) OTHER INFORMATION:

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 7245..8123
- (D) OTHER INFORMATION:

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 8333..11290
- (D) OTHER INFORMATION:

(ix) FEATURE:

- (A) NAME/KEY: CDS

- (B) LOCATION: 11098..12402
(D) OTHER INFORMATION:
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 12510..13598
(D) OTHER INFORMATION:
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 13792..15291
(D) OTHER INFORMATION:
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 15298..16080
(D) OTHER INFORMATION:
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 16129..17013
(D) OTHER INFORMATION:
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: complement (17380..18216)
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GGATCCCGAA GAGCTCTCCC AGAAGTTTTT CTTTTCGGAC GTATCGGAGG ACGAAGAACC	60
GGCACGCGGG AGGAGCTGGA GCGACCCGGA GTCGGAGGAA GAGCAGCCTG GGTGCCGGGG	120
ACTGGACTTG GCGAGGAGG ACACGGGACA CAGCTCCACC GAGTCAGAGC CCACGCAATC	180
TGACTTAGAC TTTATTGACG ACAGCTCTCC GGCGCCGCCG CCATTTGCTA TCCCCGCGT	240
CCGTGCGTTA TTGCGGTGCG CGGCACCCGC AAAGACCCAC GGAAGGCTTC GGCCGCCAGG	300
GCGGGTAGGC GCACTCTTAA AAGACGGAGG TTGTCATTTT CTTCTTCCTC TGACGAGGAA	360
TCCGAGGAGA GAAGTAAAAA AGAAGAAGCG GCCTCGACCC CTGCACGGCG ACGCAAGGCC	420
GAGGCCTCGA CGAGCAGATA GAGGAGACGC GGGGCAGAAC CTCCCCCTCC CTCCCACCCC	480
CCTACTCTGG ACATTTATTG CCCGCTCGAT CCATTCTCAT CCAGAACTTC TTTCCCGCTC	540
AGCCTTCACG CAGAAGCGGA CGCGCGCCCC TTTGCGACCG CCGGACATCC CGCCGCCCCC	600
CCCCCTTCAC GCCCGGCGCA ATCCGTAGCC GTCCAACCTCG GCCCAGCACA ACCGCAGTAG	660
ACCGCCCGGA CCGCTCTCCT CTAGACACAT CCCTAA ATG GAA AAC ATG CTC GAC	714
Met Glu Asn Met Leu Asp	
1 5	
GGG TGC TAC CCG CTG GCG CTG ATG GAC AGC GAT CAC ATT ACT GCG CAC	762
Gly Cys Tyr Pro Leu Ala Leu Met Asp Ser Asp His Ile Thr Ala His	
10 15 20	
GCG GTA CCT CGT GGC GAG CGC AGG CGG CAA GGT GCC GCT GTC GCC TCG	810
Ala Val Pro Arg Gly Glu Arg Arg Arg Gln Gly Ala Ala Val Ala Ser	
25 30 35	
TCG GAG TCG GCC GAC TCG GTA GAC CCG TGC ATT CGG ATC GCC TCG CGG	858
Ser Glu Ser Ala Asp Ser Val Asp Pro Cys Ile Arg Ile Ala Ser Arg	
40 45 50	
CTC TGG CGC GAG TTA GTC GAG ATA TCG TCC GAA CTC AAG GAC GGT TAC	906
Leu Trp Arg Glu Leu Val Glu Ile Ser Ser Glu Leu Lys Asp Gly Tyr	
55 60 65 70	

GGA GAG TTC ACG TCA GCG AGA GAC CGC CGC AAC GCG CTG ATT GCT GCC Gly Glu Phe Thr Ser Ala Arg Asp Arg Asn Ala Leu Ile Ala Ala 75 80 85	954
AAC GAA CGG CTA CGT TCG GCT TTT CTG GGG GCC AGC CGG GCG ACG CGC Asn Glu Arg Leu Arg Ser Ala Phe Leu Gly Ala Ser Arg Ala Thr Arg 90 95 100	1002
GGC CTA GGT TTG AGG CCG CGG TGG GCG TCG ACG GAG AGC GTC GCC AAC Gly Leu Gly Leu Arg Pro Arg Trp Ala Ser Thr Glu Ser Val Ala Asn 105 110 115	1050
TCC CCC ACT GAC CCG AAT AAC GGC AAC GGG TTG GGA GAA TTA GAG GAG Ser Pro Thr Asp Pro Asn Asn Gly Asn Gly Leu Gly Glu Leu Glu Glu 120 125 130	1098
GCA ATG GAA GGG ATC GAG GGC GAT TTC TGG CTC GAC TCT CTG GAC GGT Ala Met Glu Gly Ile Glu Gly Asp Phe Trp Leu Asp Ser Leu Asp Gly 135 140 145 150	1146
GAC CGC TTC GAG GAC GAG AGC CGT ACC ATG CAG AGC GAG AAT ATG CGT Asp Arg Phe Glu Asp Glu Ser Arg Thr Met Gln Ser Glu Asn Met Arg 155 160 165	1194
TTC GTG ATC GAG AAA GAA CTG TTA TCC TGG CTG TCC CGA CAC CTG CCG Phe Val Ile Glu Lys Glu Leu Leu Ser Trp Leu Ser Arg His Leu Pro 170 175 180	1242
GCC GAC CTC GCG TCC GCC GAG CGA GAG ACC TCC CGG TCT CTC CTG GCG Ala Asp Leu Ala Ser Ala Glu Arg Glu Thr Ser Arg Ser Leu Leu Ala 185 190 195	1290
GCC GGG CAC TGG TGC TGC TTG TGG CAC CCT CGG CCG TGC CGC GAA GCG Ala Gly His Trp Cys Cys Leu Trp His Pro Arg Pro Cys Arg Glu Ala 200 205 210	1338
TGT TTG TAC GAC TCG ATT TAC GTG CAG AGT CTT TTC TGC GTC GGG ACG Cys Leu Tyr Asp Ser Ile Tyr Val Gln Ser Leu Phe Cys Val Gly Thr 215 220 225 230	1386
GGG AGA GTC CCG CAA TCG GAG ATG CGC CGT CGC GAA TAC CTG GCC GCC Gly Arg Val Pro Gln Ser Glu Met Arg Arg Arg Glu Tyr Leu Ala Ala 235 240 245	1434
TTG CGC GCC GGC GCG GCT GCC GCC AAC TCT CCC GAA GTG AGC GCC TCG Leu Arg Ala Gly Ala Ala Ala Ala Asn Ser Pro Glu Val Ser Ala Ser 250 255 260	1482
ATC TTT GCG AGG GAC GCT GGA ATC GCG CTG GCG CTG GCG CGG CGC CGT Ile Phe Ala Arg Asp Ala Gly Ile Ala Leu Ala Leu Ala Arg Arg Arg 265 270 275	1530
TGA CGGGAGAATG ACGCCCTCTA GCGGCTTCCT TACCTCCGCG TCCCTGACAA	1583
CCTCGCGGGT TTTTACACTG TCCTCCGTCC ACTCTCCCC CTCACCCACT CCGCGGCAGC	1643
GAAACACAAC CCCCCCCCCC CCCAGAAAC GAGCGACACG CGAGCGCTGC GAAATAAATA	1703
AAGTAATATT ATTGTGTGTT TTTCACGTTG TTGCAATCGA GAGGCCGTTT GTCTGTCTGT	1763
GTCTGTGCGG AGCTAGGCTT TCCCGGGCGG CCCCGTTCCA CCGTTCGGTT AGGCCGGTGG	1823
CGACGGGACA TAGAGAAAGA TAGAGCGCGC GCCCTGGCGG CGAGAGGGTG TTGCGGGGGT	1883
AAATGGGACC CTGAGCTCAC CATTTTGGCG GGGGATTGCA CGGGTAACAA AAAGCTCTCT	1943

CGCACATAAT GATTTCCCTT AAACAGTGGC TGTAAGAGCT TTCTTCGACT GGGACGCGCA 2003
CGTCCGGAGA CATGATCTTA TCGGTAGCTA CACAGTTCAT GAGGTGGGCC ACGAACGCGC 2063
GGATCGAGTT TTGGGAACCT TCGGGGAGGT CTTCCGGGAG GGTGAAGTTT GACAGAGGCA 2123
GCGCTATCAC CAGGAGGCTC CGCACCATCT CCATGCCTAT CTTATCGCC GCGAGTCCGG 2183
CGGCCGGCGC GCTGCTCTGG TTATTCCAGT GCGCGGACCG CGAGTGCGCC CCTCCCCGGG 2243
CTCTGATATA GAGCACCGGC AGCTCGACGG CGGCGGAGAA AAAAGAAAGA ATGTCCGGCC 2303
CAATGACTGG AACTTTGGGC ACGTCTCTTA TTTCCACGC GGCGGCCCCG GGAATCTGCT 2363
TGCCCCAGAC CTTGCTTTCC AACTCCCCGT TCGGCCCCC AACTAACTCC GACAGCGCGG 2423
TCCACAGTCC TACCGCCGCT GCGACGGCGC GCTTAGCCGC GGGCGCTATT CGCGGGTCGT 2483
GCGCCGTGAT ATCTTCGGCG ACCTGCAGAC TGCCAGCCT TTCCTTCCCT TCAAAATACG 2543
CGCGGGCGGC CTGTACGATC ACCGCGGCCA GATCGGGCCA AAAGAAAATA TCGCAACTCT 2603
GCGACGCCCC CCAGAATCTC CCTCCGGGCA GGTCCGTGCC CCTAAAGGCC GCCGAGAAAG 2663
CTAAGTCCAA ATGTGACGTC GGAGGTCTCG ACATGGTCGC CAACCCTCCA AATGCTACCC 2723
GCCGGCCCCAC GCAACGCGGG CTTTTATAAA GATGGCGCGC GAGACAATAA CACTTACTCA 2783
TCCGCGTACG CGTTTATTAT TGTCAATATT TGTGTGGTTA TTATTACTGC TACCGCCCTT 2843
GTTTCTGCAA GGCCCTCGCC GCGGCCAGG CCACTATTCC GGCAGCGGCC GCCGACGCGG 2903
CGAGCGTCGC CGCTAACGTC GGCGCCGCGG GGAGCGGGGT TTCTTCGACT TAAATAGACT 2963
CCCGAGAAAA AATTTTGGCT GCCGTCGCC ATCATCCGAG TCGGAAACAC AGTATGCGGC 3023
CGAGTTAGGT TTTACTTTTA AAACTTTAC CGTGCTGTAC GGCCAGGGCG TTCTCAGGCT 3083
CGAAGGGGCA AGAGTTGTCC AGACTGATGG GTGACTCAGA GACAGCGTTG TCTTGTCTCC 3143
GTTTACCAA AATATTTCCA CTCCTCTCTC AAAATTTTTA CCTCCGGTTT CGGTAATTAG 3203
GAAAGTTTTT GCGCAGGGA GGTTTAAAGC TGCCATGCAT ATGTCAGCGG TACCCAGCAC 3263
CCACAAATGG AACTCTTTTG CGGCATACGC GCCAGATGAC AAATGGTAAA ACCCTGCGTC 3323
CAAGCCGCTC CACTCGGGAC TTA CTCCAGG CGGGTCGCCC CCTCACC GAACCAATCAC 3383
GGGTCTGCAC ATCCTGGGAA GGGAAAACAG CTCCCGGAA ACTTCGTACA GAGATGCCGG 3443
GCGCACGATT ACCGATAATG TACTCGGACG ATCGTAACTC GCCATAGTTT TCACTGCGTG 3503
AACCAATTCT TTCCATCCAG AATCCGAGAG CTCAAATCTA GAATTAGGTA GTTTGTAGTG 3563
CGAATCGACC GCAGAACTA TAGTCACTTT TACAGGCGCC ATCGCCGCTCAG 3615
ACTCCACCCC GCTATGATGT CAGAAATATA ACGCTCTTAT TCTAGCAGAG TCAGGCCAAT 3675
ATATACAGCT TAGAGAAG ATG CGG TTT CGG CGC ATC TGT TCA CGC TCT AGG 3726
Met Arg Phe Arg Arg Ile Cys Ser Arg Ser Arg
1 5 10
GCA GAA AAA CGA AGA AGA ACA ACC GAG AAT CCG CTT ACC TCA AAA CGC 3774
Ala Glu Lys Arg Arg Arg Thr Thr Glu Asn Pro Leu Thr Ser Lys Arg
15 20 25

GTT TGC GTA TTG GAT AGT TTC TCA CGG ACA ATG TCA TTG CGC CCC TAT Val Cys Val Leu Asp Ser Phe Ser Arg Thr Met Ser Leu Arg Pro Tyr 30 35 40	3822
GCA GAA ATT TTG CCG ACC GCG GAA GGC GTC GAG CGC CTC GCC GAA CTT Ala Glu Ile Leu Pro Thr Ala Glu Gly Val Glu Arg Leu Ala Glu Leu 45 50 55	3870
GTT AGT GTG ACA ATG ACA GAA CGC GCG GAA CCT GTG ACA GAG AAT ACA Val Ser Val Thr Met Thr Glu Arg Ala Glu Pro Val Thr Glu Asn Thr 60 65 70 75	3918
GCT GTA AAC AGT ATC CCC CCG GCT AAC GAG AAC GGG CAG AAC TTC GCA Ala Val Asn Ser Ile Pro Pro Ala Asn Glu Asn Gly Gln Asn Phe Ala 80 85 90	3966
TAT GCA GGC GAT GGG CCC TCG ACT ACT GAA AAA GTT GAC GGC TCG CAT Tyr Ala Gly Asp Gly Pro Ser Thr Thr Glu Lys Val Asp Gly Ser His 95 100 105	4014
ACA GAC TTC GAT GAA GCA TCG AGC GAC TAC GCC GGC CCT GTC CCG CTC Thr Asp Phe Asp Glu Ala Ser Ser Asp Tyr Ala Gly Pro Val Pro Leu 110 115 120	4062
GCG CAA ACT AGA TTG AAG CAT TCG GAT GAA TTT CTT CAG CAC TTC CGA Ala Gln Thr Arg Leu Lys His Ser Asp Glu Phe Leu Gln His Phe Arg 125 130 135	4110
GTT TTA GAC GAT TTG GTG GAG GGG GCT TAC GGG TTT ATC TGC GAC GTC Val Leu Asp Asp Leu Val Glu Gly Ala Tyr Gly Phe Ile Cys Asp Val 140 145 150 155	4158
CGT CGC TAC ACC GAG GAA GAG CAA CGT CGA AGA GGG GTT AAC AGT ACT Arg Arg Tyr Thr Glu Glu Gln Arg Arg Arg Gly Val Asn Ser Thr 160 165 170	4206
AAC CAG GGG AAA TCA AAA TGT AAG CGC CTG ATA GCT AAA TAT GTG AAA Asn Gln Gly Lys Ser Lys Cys Lys Arg Leu Ile Ala Lys Tyr Val Lys 175 180 185	4254
AAT GGA ACA AGG GCG GCC TCT CAG CTG GAA AAT GAA ATT TTG GTT CTC Asn Gly Thr Arg Ala Ala Ser Gln Leu Glu Asn Glu Ile Leu Val Leu 190 195 200	4302
GGG CGC CTA AAT CAC GAG AAT GTT CTC AAG ATC CAG GAA ATC CTT CGG Gly Arg Leu Asn His Glu Asn Val Leu Lys Ile Gln Glu Ile Leu Arg 205 210 215	4350
TAC CCG GAT AAT ACG TAC ATG TTA ACG CAG AGG TAT CAG TTC GAC TTG Tyr Pro Asp Asn Thr Tyr Met Leu Thr Gln Arg Tyr Gln Phe Asp Leu 220 225 230 235	4398
TAC AGC TAC ATG TAC GAT GAA GCG TTC GAC TGG AAA GAC AGT CCA ATG Tyr Ser Tyr Met Tyr Asp Glu Ala Phe Asp Trp Lys Asp Ser Pro Met 240 245 250	4446
CTT AAA CAG ACT AGA CGC ATC ATG AAG CAG CTC ATG TCA GCG GTC TCG Leu Lys Gln Thr Arg Arg Ile Met Lys Gln Leu Met Ser Ala Val Ser 255 260 265	4494
TAT ATC CAT TCA AAG AAA CTG ATT CAC AGG GAC ATC AAA CTC GAA AAT Tyr Ile His Ser Lys Lys Leu Ile His Arg Asp Ile Lys Leu Glu Asn 270 275 280	4542
ATT TTC TTA AAC TGC GAC GGC AAG ACA GTG CTG GGC GAC TTT GGA ACT Ile Phe Leu Asn Cys Asp Gly Lys Thr Val Leu Gly Asp Phe Gly Thr 285 290 295	4590

GTC ACG CCT TTT GAA AAT GAG CGG GAG CCC TTC GAA TAT GGA TGG GTG Val Thr Pro Phe Glu Asn Glu Arg Glu Pro Phe Glu Tyr Gly Trp Val 300 305 310 315	4638
GGG ACC GTG GCT ACT AAC TCT CCC GAG ATA CTC GCC AGG GAT TCG TAC Gly Thr Val Ala Thr Asn Ser Pro Glu Ile Leu Ala Arg Asp Ser Tyr 320 325 330	4686
TGT GAA ATT ACA GAC ATT TGG AGC TGC GGA GTA GTA TTG CTG GAA ATG Cys Glu Ile Thr Asp Ile Trp Ser Cys Gly Val Val Leu Leu Glu Met 335 340 345	4734
GTA AGC CAT GAA TTT TGC CCG ATC GGC GAT GGC GGG GGA AAT CCG CAC Val Ser His Glu Phe Cys Pro Ile Gly Asp Gly Gly Asn Pro His 350 355 360	4782
CAG CAA TTG CTG AAA GTT ATC GAC TCT CTC TCA GTT TGT GAT GAA GAG Gln Gln Leu Leu Lys Val Ile Asp Ser Leu Ser Val Cys Asp Glu Glu 365 370 375	4830
TTC CCA GAC CCC CCG TGT AAT CTG TAC AAT TAT TTG CAT TAT GCG AGC Phe Pro Asp Pro Pro Cys Asn Leu Tyr Asn Tyr Leu His Tyr Ala Ser 380 385 390 395	4878
ATC GAT CGC GCC GGA CAT ACG GTC CCG TCG CTC ATA CGG AAC CTC CAC Ile Asp Arg Ala Gly His Thr Val Pro Ser Leu Ile Arg Asn Leu His 400 405 410	4926
CTT CCG GCG GAT GTG GAA TAC CCT CTA GTT AAA ATG CTT ACT TTT GAC Leu Pro Ala Asp Val Glu Tyr Pro Leu Val Lys Met Leu Thr Phe Asp 415 420 425	4974
TGG CGT TTG AGA CCC AGC GCG GCC GAA GTA TTG GCA ATG CCA CTG TTT Trp Arg Leu Arg Pro Ser Ala Ala Glu Val Leu Ala Met Pro Leu Phe 430 435 440	5022
TCG GCT GAA GAG GAA CGG ACC ATA ACA ATT ATT CAT GGA AAA CAT AAA Ser Ala Glu Glu Glu Arg Thr Ile Thr Ile Ile His Gly Lys His Lys 445 450 455	5070
CCC ATC CGA CCC GAA ATC CGT GCG CGG GTG CCA CGG TCC ATG AGT GAA Pro Ile Arg Pro Glu Ile Arg Ala Arg Val Pro Arg Ser Met Ser Glu 460 465 470 475	5118
GGT TAA TAATAAAGGA CGGAGATAGA GAACTGAAGC GTCAGATTTT TTTAAAAAAA Gly	5174
TAAATGATCG AGAACTTATG ATTTGTCTTT CTTGA ATG ACC TTG CCC CAT CGA Met Thr Leu Pro His Arg 1 5	5227
TTA ACG AAA AGA CCT TTC GCG CGT CGA TTC TGC TCG GTC TTT GTG ATA Leu Thr Lys Arg Pro Phe Ala Arg Arg Phe Cys Ser Val Phe Val Ile 10 15 20	5275
CAT TAT AGT GAG ACT AAA CTC GAC CGA TAT AAC AAG ACA ATG TTA CTC His Tyr Ser Glu Thr Lys Leu Asp Arg Tyr Asn Lys Thr Met Leu Leu 25 30 35	5323
TAT AGA CCG GAC TCA ACC ATG CGG CAT AGC GGA GGC GAC GCA AAT CAC Tyr Arg Pro Asp Ser Thr Met Arg His Ser Gly Gly Asp Ala Asn His 40 45 50	5371
AGA GGG ATA AGG CCG AGG CGG AAA TCT ATT GGA GCG TTT AGC GCG CGC Arg Gly Ile Arg Pro Arg Arg Lys Ser Ile Gly Ala Phe Ser Ala Arg 55 60 65 70	5419

GAA AAG ACT GGA AAA CGA AAT GCG CTG ACG GAA AGC AGC TCC TCC TCC Glu Lys Thr Gly Lys Arg Asn Ala Leu Thr Glu Ser Ser Ser Ser Ser	5467
GAC ATG CTA GAT CCG TTT TCC ACG GAT AAG GAA TTT GGC GGT AAG TGG Asp Met Leu Asp Pro Phe Ser Thr Asp Lys Glu Phe Gly Gly Lys Trp	5515
ACG GTA GAC GGA CCT GCC GAC ATT ACT GCC GAG GTC CTT TCT CAG GCA Thr Val Asp Gly Pro Ala Asp Ile Thr Ala Glu Val Leu Ser Gln Ala	5563
TGG GAC GTT CTC CAA TTA GTG AAG CAT GAA GAT GCG GAG GAG GAG AGA Trp Asp Val Leu Gln Leu Val Lys His Glu Asp Ala Glu Glu Glu Arg	5611
GTG ACT TAT GAG TCC AAA CCG ACC CCG ATA CAG CCG TTC AAT GCC TGG Val Thr Tyr Glu Ser Lys Pro Thr Pro Ile Gln Pro Phe Asn Ala Trp	5659
CCG GAC GGG CCG AGT TGG AAC GCG CAG GAT TTT ACT CGA GCG CCA ATA Pro Asp Gly Pro Ser Trp Asn Ala Gln Asp Phe Thr Arg Ala Pro Ile	5707
GTT TAT CCC TCT GCG GAG GTA TTG GAC GCA GAG GCG TTG AAA GTA GGG Val Tyr Pro Ser Ala Glu Val Leu Asp Ala Glu Ala Leu Lys Val Gly	5755
GCA TTC GTT AGC CGA GTT TTA CAA TGT GTA CCG TTC ACG CGA TCA AAG Ala Phe Val Ser Arg Val Leu Gln Cys Val Pro Phe Thr Arg Ser Lys	5803
AAA AGC GTT ACG GTG CGG GAT GCG CAG TCG TTT TTG GGG GAC TCG TTC Lys Ser Val Thr Val Arg Asp Ala Gln Ser Phe Leu Gly Asp Ser Phe	5851
TGG AGA ATA ATG CAG AAC GTT TAC ACG GTT GTC TTA CGA CAG CAC ATA Trp Arg Ile Met Gln Asn Val Tyr Thr Val Val Leu Arg Gln His Ile	5899
ACT CGA CTC AGG CAC CCT TCC AGC AAA AGC ATT GTT AAC TGC AAC GAC Thr Arg Leu Arg His Pro Ser Ser Lys Ser Ile Val Asn Cys Asn Asp	5947
CCT CTA TGG TAC GCC TAC GCG AAT CAA TTT CAC TGG AGA GGA ATG CGC Pro Leu Trp Tyr Ala Tyr Ala Asn Gln Phe His Trp Arg Gly Met Arg	5995
GTG CCG TCG CTT AAA TTA GCC TCT CCC CCG GAG GAG AAT ATT CAA CAC Val Pro Ser Leu Lys Leu Ala Ser Pro Pro Glu Glu Asn Ile Gln His	6043
GGC CCA ATG GCC GCC GTT TTT AGA AAC GCG GGG GCT GGT CTG TTC CTG Gly Pro Met Ala Ala Val Phe Arg Asn Ala Gly Ala Gly Leu Phe Leu	6091
TGG CCT GCC ATG CGC GCA GCC TTT GAA GAG CGC GAC AAG CGA CTG TTA Trp Pro Ala Met Arg Ala Ala Phe Glu Glu Arg Asp Lys Arg Leu Leu	6139
AGA GCA TGC CTG TCT TCA CTC GAT ATC ATG GAC GCA GCC GTC CTC GCG Arg Ala Cys Leu Ser Ser Leu Asp Ile Met Asp Ala Ala Val Leu Ala	6187
TCG TTT CCA TTT TAC TGG CGC GGC GTC CAA GAC ACC TCG CGC TTC GAG Ser Phe Pro Phe Tyr Trp Arg Gly Val Gln Asp Thr Ser Arg Phe Glu	6235

CCT GCG CTG GGC TGT TTG TCA GAG TAC TTT GCA CTA GTG GTG TTA CTG Pro Ala Leu Gly Cys Leu Ser Glu Tyr Phe Ala Leu Val Val Leu Leu 345 350 355	6283
GCC GAG ACG GTC TTA GCG ACC ATG TTC GAC CAC GCA CTG GTA TTC ATG Ala Glu Thr Val Leu Ala Thr Met Phe Asp His Ala Leu Val Phe Met 360 365 370	6331
AGG GCG CTG GCA GAC GGC AAT TTC GAT GAC TAT GAC GAA ACT AGA TAT Arg Ala Leu Ala Asp Gly Asn Phe Asp Asp Tyr Asp Glu Thr Arg Tyr 375 380 385 390	6379
ATA GAC CCC GTT AAA AAC GAG TAC CTG AAC GGA GCC GAG GGT ACT CTG Ile Asp Pro Val Lys Asn Glu Tyr Leu Asn Gly Ala Glu Gly Thr Leu 395 400 405	6427
TTA CGG GGC ATA GTG GCC TCC AAC ACC GCT CTG GCG GTG GTT TGC GCA Leu Arg Gly Ile Val Ala Ser Asn Thr Ala Leu Ala Val Val Cys Ala 410 415 420	6475
AAC ACC TAT TCG ACG ATA AGA AAA CTC CCG TCC GTG GCA ACT AGC GCG Asn Thr Tyr Ser Thr Ile Arg Lys Leu Pro Ser Val Ala Thr Ser Ala 425 430 435	6523
TGC AAT GTT GCC TAC AGG ACC GAA ACG CTG AAA GCG AGG CGC CCT GGC Cys Asn Val Ala Tyr Arg Thr Glu Thr Leu Lys Ala Arg Arg Pro Gly 440 445 450	6571
ATG AGC GAC ATA TAC CGG ATA TTA CAA AAA GAG TTT TTC TTT TAC ATT Met Ser Asp Ile Tyr Arg Ile Leu Gln Lys Glu Phe Phe Phe Tyr Ile 455 460 465 470	6619
GCG TGG CTC CAG AGG GTT GCA ACA CAC GCA AAT TTC TGT TTA AAC ATT Ala Trp Leu Gln Arg Val Ala Thr His Ala Asn Phe Cys Leu Asn Ile 475 480 485	6667
CTG AAG AGA AGC GTG GAT ACG GGG GCC CCG CCA TTT TTG TTC AGG GCC Leu Lys Arg Ser Val Asp Thr Gly Ala Pro Pro Phe Leu Phe Arg Ala 490 495 500	6715
AGC TCG GAG AAG CGG CTG CAG CAG TTA AAT AAA ATG CTC TGC CCC CTT Ser Ser Glu Lys Arg Leu Gln Gln Leu Asn Lys Met Leu Cys Pro Leu 505 510 515	6763
CTC GTG CCG ATT CAA TAT GAA GAC TTT TCG AAG GCC ATG GGG TCT GAG Leu Val Pro Ile Gln Tyr Glu Asp Phe Ser Lys Ala Met Gly Ser Glu 520 525 530	6811
CTC AAG AGG GAA AAG TTA GAG ACA TTC GTT AAA GCT ATT TCC AGC GAC Leu Lys Arg Glu Lys Leu Glu Thr Phe Val Lys Ala Ile Ser Ser Asp 535 540 545 550	6859
AGG GAC CCG AGG GGG TCC TTA AGA TTT CTC ATT TCG GAC CAT GCA AGG Arg Asp Pro Arg Gly Ser Leu Arg Phe Leu Ile Ser Asp His Ala Arg 555 560 565	6907
GAA ATT ATT GCA GAC GGA GTA CGG TTT AAG CCG GTG ATA GAC GAG CCG Glu Ile Ile Ala Asp Gly Val Arg Phe Lys Pro Val Ile Asp Glu Pro 570 575 580	6955
GTT CGG GCT TCA GTT GCG CTG AGT ACC GCT GCC GCT GGG AAA GTG AAA Val Arg Ala Ser Val Ala Leu Ser Thr Ala Ala Ala Gly Lys Val Lys 585 590 595	7003
GCG CGA CGC TTA ACC TCA GTT CGC GCG CCC GTA CCG GGC GCA GGC GCC Ala Arg Arg Leu Thr Ser Val Arg Ala Pro Val Pro Gly Ala Gly Ala 600 605 610	7051

GTT TCC GCG CGC CGG AAA TCG GAA ATA TGA TAAAAATGCT TGGCATTGCT	7101
Val Ser Ala Arg Arg Lys Ser Glu Ile	
615 620	
GGGCGAAGAG GCGTGATCTG AAGGGCTCCA CAATGACGTA ACTGAGCTAC GCATCCCTAT	7161
AAAGTGTACC CGCTGACCGC TAGCCCATAC AGTGTTACAG GAGGGGAGAG AGACAACTTC	7221
AGCTCGAAGT CTGAAGAGAC ATC ATG AGC GGC TTC AGT AAC ATA GGA TCG	7271
Met Ser Gly Phe Ser Asn Ile Gly Ser	
1 5	
ATT GCC ACC GTT TCC CTA GTA TGC TCG CTT TTG TGC GCA TCT GTA TTA	7319
Ile Ala Thr Val Ser Leu Val Cys Ser Leu Leu Cys Ala Ser Val Leu	
10 15 20 25	
GGG GCG CCG GTA CTG GAC GGG CTC GAG TCG AGC CCT TTC CCG TTC GGG	7367
Gly Ala Pro Val Leu Asp Gly Leu Glu Ser Ser Pro Phe Pro Phe Gly	
30 35 40	
GGC AAA ATT ATA GCC CAG GCG TGC AAC CGC ACC ACG ATT GAG GTG ACG	7415
Gly Lys Ile Ile Ala Gln Ala Cys Asn Arg Thr Thr Ile Glu Val Thr	
45 50 55	
GTC CCG TGG AGC GAC TAC TCT GGT CGC ACC GAA GGA GTG TCA GTC GAG	7463
Val Pro Trp Ser Asp Tyr Ser Gly Arg Thr Glu Gly Val Ser Val Glu	
60 65 70	
GTG AAA TGG TTC TAC GGG AAT AGT AAT CCC GAA AGC TTC GTG TTC GGG	7511
Val Lys Trp Phe Tyr Gly Asn Ser Asn Pro Glu Ser Phe Val Phe Gly	
75 80 85	
GTG GAT AGC GAA ACG GGC AGT GGA CAC GAG GAC CTG TCT ACG TGC TGG	7559
Val Asp Ser Glu Thr Gly Ser Gly His Glu Asp Leu Ser Thr Cys Trp	
90 95 100 105	
GCT CTA ATC CAT AAT CTG AAC GCG TCT GTG TGC AGG GCG TCT GAC GCC	7607
Ala Leu Ile His Asn Leu Asn Ala Ser Val Cys Arg Ala Ser Asp Ala	
110 115 120	
GGG ATA CCT GAT TTC GAC AAG CAG TGC GAA AAA GTG CAG AGA AGA CTG	7655
Gly Ile Pro Asp Phe Asp Lys Gln Cys Glu Lys Val Gln Arg Arg Leu	
125 130 135	
CGC TCC GGG GTG GAA CTT GGT AGT TAC GTG TCT GGC AAT GGA TCC CTG	7703
Arg Ser Gly Val Glu Leu Gly Ser Tyr Val Ser Gly Asn Gly Ser Leu	
140 145 150	
GTG CTG TAC CCA GGG ATG TAC GAT GCC GGC ATC TAC GCC TAC CAG CTC	7751
Val Leu Tyr Pro Gly Met Tyr Asp Ala Gly Ile Tyr Ala Tyr Gln Leu	
155 160 165	
TCA GTG GGT GGG AAG GGA TAT ACC GGG TCT GTT TAT CTA GAC GTC GGA	7799
Ser Val Gly Gly Lys Gly Tyr Thr Gly Ser Val Tyr Leu Asp Val Gly	
170 175 180 185	
CCA AAC CCC GGA TGC CAC GAC CAG TAT GGG TAC ACC TAT TAC AGC CTG	7847
Pro Asn Pro Gly Cys His Asp Gln Tyr Gly Tyr Thr Tyr Tyr Ser Leu	
190 195 200	
GCC GAC GAG GCG TCA GAC TTA TCA TCT TAT GAC GTA GCC TCG CCC GAA	7895
Ala Asp Glu Ala Ser Asp Leu Ser Ser Tyr Asp Val Ala Ser Pro Glu	
205 210 215	
CTC GAC GGT CCT ATG GAG GAA GAT TAT TCC AAT TGT CTA GAC ATG CCC	7943
Leu Asp Gly Pro Met Glu Glu Asp Tyr Ser Asn Cys Leu Asp Met Pro	
220 225 230	

[illegible]

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TCAGACTCCG AGTACTGAAC AGGCGGCTCT TACTCAGACG CAGATCGCAG AAACGGAGGC	9813
GTTGTTTACT CAGACTCCGA GTGCTGAACA GATGACTTTT ACTCAGACTC CGGGTGCAGA	9873
AACCGAGGCA CCTGCCCAGA CCCCAGCAC GATACCCGAG ATATTTACTC AGTCTCGTAG	9933
CACGCCCCC GAAACCGCTC GCGCTCCGAG CGCGGCGCCG GAGGTTTTTA CACAGAGTTC	9993
GAGTACGGTA ACGGAGGTGT TTACTCAGAC CCCGAGCACG GTACCGAAAA CTACTCTGAG	10053
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TCAGACTTCG AGTGCCGAGC CGGACACTAT GCGAACTCAG AGTACTGAAA CACACTTTTT	10173
CACTCAGGCC CCGAGTACGG TACCGAAAGC TACTCAGACT CCGAGTACAG AGCCGGAGGT	10233
GTTGACTCAG AGTCCGAGTA CCGAACCTGT GCCTTTCACC CGGACTCTGG GCGCAGAGCC	10293
GGAAATTACT CAGACCCCGA GCGCGGCACC GGAGGTTTAT ACTCGGAGTT CGAGTACGAT	10353
GCCAGAACT GCACAGAGCA CACCCCTGGC CTCGCAAAAC CCTACCAGTT CGGGAACCGG	10413
GACGCATAAT ACTGAACCGA GGAATTATCC AGTGCAACG ACACCACATA CCCAGAACT	10473
CTACACAGAA AATAAGACTT TATCGTTTCC TACTGTTGTT TCAGAATTCC ATGAGATGTC	10533
GACGGCAGAG TCGCAGACGC CCCTATTGGA CGTCAAAATT GTAGAGGTGA AGTTTTCAAA	10593
CGATGGCGAA GTAACGGCGA CTTGCGTTTC CACCGTCAAA TCTCCCTATA GGGTAGAAAC	10653
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AACATCGGTC CAGCTAATGT GCCTGTCGTG CACGAGCCAT TCTCCGGAAC CTTACTGTCT	10833
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TGGCCGGGGA GGCAATATAT ACGAATGCAC CGTCCTCATC TCAGACGGCA CTCGCGTTAC	11133
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GGCGCAGCTG TATTCACTCT TTTCTGGA CTGTGTCAGGA TTATGCGGGA GCATATCTGC	11253
TTTGTACGCA ACGCTATGGA CCGCCATTTA TTTTGA GGAATGCTTT TTGGAATATC	11310
GTACTGCTTT CTTCCTTCGC TAGCCAGAGC ACCGCCGCCG TCACGTACGA CTACATTTTA	11370
GGCCGTGCG CGCTCGACGC GCTAACCATA CCGGCGGTTG GCGCGTATAA CAGATACCTC	11430
ACTAGGGTAT CAAGAGGCTG CGACGTTGTC GAGCTCAACC CGATTTCTAA CGTGGACGAC	11490
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TACAGGGAAT GTGGCGACGT ACAACTGCTA TCTGAATGCG CCGTTCAATC TGCACAGATG	11670
TGGGCAGTGG ACTATGTTCC TAGCACCTTT GTATCGCGAA ATGGCGCGGG ACTGACTATA	11730

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TTCTCCCCCA CTGCTGCGCT CTCTGGCCAA TACTTGCTGA CCCTGAAAAT CGGGAGATT 11790
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 Leu Ala Pro Phe Gly Ala Met Gly Ile Val Ile Thr Gly Asn His Val
 15 20 25 30
 TCC GCC AGG ATT GAC GAC GAT CAC ATC GTG ATC GTC GCG CCT CGC CCC 12647
 Ser Ala Arg Ile Asp Asp Asp His Ile Val Ile Val Ala Pro Arg Pro
 35 40 45
 GAA GCT ACA ATT CAA CTG CAG CTA TTT TTC ATG CCT GGC CAG AGA CCC 12695
 Glu Ala Thr Ile Gln Leu Gln Leu Phe Phe Met Pro Gly Gln Arg Pro
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 CAC AAA CCC TAC TCA GGA ACC GTC CGC GTC GCG TTT CGG TCT GAT ATA 12743
 His Lys Pro Tyr Ser Gly Thr Val Arg Val Ala Phe Arg Ser Asp Ile
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 ACA AAC CAG TGC TAC CAG GAA CTT AGC GAG GAG CGC TTT GAA AAT TGC 12791
 Thr Asn Gln Cys Tyr Gln Glu Leu Ser Glu Glu Arg Phe Glu Asn Cys
 80 85 90
 ACT CAT CGA TCG TCT TCT GTT TTT GTC GGC TGT AAA GTG ACC GAG TAC 12839
 Thr His Arg Ser Ser Ser Val Phe Val Gly Cys Lys Val Thr Glu Tyr
 95 100 105 110
 ACG TTC TCC GCC TCG AAC AGA CTA ACC GGA CCT CCA CAC CCG TTT AAG 12887
 Thr Phe Ser Ala Ser Asn Arg Leu Thr Gly Pro Pro His Pro Phe Lys
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 CTC ACT ATA CGA AAT CCT CGT CCG AAC GAC AGC GGG ATG TTC TAC GTA 12935
 Leu Thr Ile Arg Asn Pro Arg Pro Asn Asp Ser Gly Met Phe Tyr Val
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 ATT GTT CGG CTA GAC GAC ACC AAA GAA CCC ATT GAC GTC TTC GCG ATC 12983
 Ile Val Arg Leu Asp Asp Thr Lys Glu Pro Ile Asp Val Phe Ala Ile
 145 150 155

CAA CTA TCG GTG TAT CAA TTC GCG AAC ACC GCC GCG ACT CGC GGA CTC Gln Leu Ser Val Tyr Gln Phe Ala Asn Thr Ala Ala Thr Arg Gly Leu 160 165 170	13031
TAT TCC AAG GCT TCG TGT CGC ACC TTC GGA TTA CCT ACC GTC CAA CTT Tyr Ser Lys Ala Ser Cys Arg Thr Phe Gly Leu Pro Thr Val Gln Leu 175 180 185 190	13079
GAG GCC TAT CTC AGG ACC GAG GAA AGT TGG CGC AAC TGG CAA GCG TAC Glu Ala Tyr Leu Arg Thr Glu Glu Ser Trp Arg Asn Trp Gln Ala Tyr 195 200 205	13127
GTT GCC ACG GAG GCC ACG ACG ACC AGC GCC GAG GCG ACA ACC CCG ACG Val Ala Thr Thr Ala Thr Thr Thr Ser Ala Glu Ala Thr Thr Pro Thr 210 215 220	13175
CCC GTC ACT GCA ACC AGC GCC TCC GAA CTT GAA GCG GAA CAC TTT ACC Pro Val Thr Ala Thr Ser Ala Ser Glu Leu Glu Ala Glu His Phe Thr 225 230 235	13223
TTT CCC TGG CTA GAA AAT GGC GTG GAT CAT TAC GAA CCG ACA CCC GCA Phe Pro Trp Leu Glu Asn Gly Val Asp His Tyr Glu Pro Thr Pro Ala 240 245 250	13271
AAC GAA AAT TCA AAC GTT ACT GTC CGT CTC GGG ACA ATG AGC CCT ACG Asn Glu Asn Ser Asn Val Thr Val Arg Leu Gly Thr Met Ser Pro Thr 255 260 265 270	13319
CTA ATT GGG GTA ACC GTG GCT GCC GTC GTG AGC GCA ACG ATC GGC CTC Leu Ile Gly Val Thr Val Ala Ala Val Val Ser Ala Thr Ile Gly Leu 275 280 285	13367
GTC ATT GTA ATT TCC ATC GTC ACC AGA AAC ATG TGC ACC CCG CAC CGA Val Ile Val Ile Ser Ile Val Thr Arg Asn Met Cys Thr Pro His Arg 290 295 300	13415
AAA TTA GAC ACG GTC TCG CAA GAC GAC GAA GAA CGT TCC CAA ACT AGA Lys Leu Asp Thr Val Ser Gln Asp Asp Glu Glu Arg Ser Gln Thr Arg 305 310 315	13463
AGG GAA TCG CGA AAA TTT GGA CCC ATG GTT GCG TGC GAA ATA AAC AAG Arg Glu Ser Arg Lys Phe Gly Pro Met Val Ala Cys Glu Ile Asn Lys 320 325 330	13511
GGG GCT GAC CAG GAT AGT GAA CTT GTG GAA CTG GTT GCG ATT GTT AAC Gly Ala Asp Gln Asp Ser Glu Leu Val Glu Leu Val Ala Ile Val Asn 335 340 345 350	13559
CCG TCT GCG CTA AGC TCG CCC GAC TCA ATA AAA ATG TGA TTAAGTCTGA Pro Ser Ala Leu Ser Ser Pro Asp Ser Ile Lys Met 355 360	13608
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ACTTAGGAGG AGAATTCAGC CGGGGAGAGC CCCTGTTGAG TAGGCTTGGG AGCATATTGC	13788
AGG ATG AAC ATG TTA GTG ATA GTT CTC GCC TCT TGT CTT GCG CGC CTA Met Asn Met Leu Val Ile Val Leu Ala Ser Cys Leu Ala Arg Leu 1 5 10 15	13836
ACT TTT GCG ACG CGA CAC GTC CTC TTT TTG GAA GGC ACT CAG GCT GTC Thr Phe Ala Thr Arg His Val Leu Phe Leu Glu Gly Thr Gln Ala Val 20 25 30	13884

CTC GGG GAA GAT GAT CCC AGA AAC GTT CCG GAA GGG ACT GTA ATC AAA Leu Gly Glu Asp Asp Pro Arg Asn Val Pro Glu Gly Thr Val Ile Lys 35 40 45	13932
TGG ACA AAA GTC CTG CGG AAC GCG TGC AAG ATG AAG GCG GCC GAT GTC Trp Thr Lys Val Leu Arg Asn Ala Cys Lys Met Lys Ala Ala Asp Val 50 55 60	13980
TGC TCT TCG CCT AAC TAT TGC TTT CAT GAT TTA ATT TAC GAC GGA GGA Cys Ser Ser Pro Asn Tyr Cys Phe His Asp Leu Ile Tyr Asp Gly Gly 65 70 75	14028
AAG AAA GAC TGC CCG CCC GCG GGA CCC CTG TCT GCA AAC CTG GTA ATT Lys Lys Asp Cys Pro Pro Ala Gly Pro Leu Ser Ala Asn Leu Val Ile 80 85 90 95	14076
TTA CTA AAG CGC GGC GAA AGC TTC GTC GTG CTG GGT TCT GGG CTA CAC Leu Leu Lys Arg Gly Glu Ser Phe Val Val Leu Gly Ser Gly Leu His 100 105 110	14124
AAC AGC AAT ATA ACT AAT ATC ATG TGG ACA GAG TAC GGA GGC CTG CTC Asn Ser Asn Ile Thr Asn Ile Met Trp Thr Glu Tyr Gly Gly Leu Leu 115 120 125	14172
TTT GAT CCT GTA ACT CGT TCG GAC GAG GGA ATC TAT TTT CGA CGG ATC Phe Asp Pro Val Thr Arg Ser Asp Glu Gly Ile Tyr Phe Arg Arg Ile 130 135 140	14220
TCT CAG CCA GAT CTG GCC ATG GAA ACT ACA TCG TAC AAC GTC AGC GTT Ser Gln Pro Asp Leu Ala Met Glu Thr Thr Ser Tyr Asn Val Ser Val 145 150 155	14268
CTT TCG CAC GTA GAC GAG AAG GCT CCA GCA CCG CAC GAG GTG GAG ATA Leu Ser His Val Asp Glu Lys Ala Pro Ala Pro His Glu Val Glu Ile 160 165 170 175	14316
GAC ACC ATC AAG CCG TCA GAG GCC CAC GCG CAC GTG GAA TTA CAA ATG Asp Thr Ile Lys Pro Ser Glu Ala His Ala His Val Glu Leu Gln Met 180 185 190	14364
CTG CCG TTT CAT GAA CTC AAC GAC AAC AGC CCC ACC TAT GTG ACC CCT Leu Pro Phe His Glu Leu Asn Asp Asn Ser Pro Thr Tyr Val Thr Pro 195 200 205	14412
GTT CTT AGA GTC TTC CCA CCG ACC GAG CAC GTA AAA TTT AAC GTT ACG Val Leu Arg Val Phe Pro Pro Thr Glu His Val Lys Phe Asn Val Thr 210 215 220	14460
TAT TCG TGG TAT GGG TTT GAT GTC AAA GAG GAG TGC GAA GAA GTG AAA Tyr Ser Trp Tyr Gly Phe Asp Val Lys Glu Glu Cys Glu Glu Val Lys 225 230 235	14508
CTG TTC GAG CCG TGC GTA TAC CAT CCT ACA GAC GGC AAA TGT CAG TTT Leu Phe Glu Pro Cys Val Tyr His Pro Thr Asp Gly Lys Cys Gln Phe 240 245 250 255	14556
CCC GCA ACC AAC CAG AGA TGC CTC ATA GGA TCT GTC TTG ATG GCG GAA Pro Ala Thr Asn Gln Arg Cys Leu Ile Gly Ser Val Leu Met Ala Glu 260 265 270	14604
TTC TTG GGC GCG GCC TCT TTG CTG GAT TGT TCC CGC GAT ACT CTA GAA Phe Leu Gly Ala Ala Ser Leu Leu Asp Cys Ser Arg Asp Thr Leu Glu 275 280 285	14652
GAC TGC CAC GAA AAT CGC GTG CCG AAC CTA CGG TTC GAT TCG CGA CTC Asp Cys His Glu Asn Arg Val Pro Asn Leu Arg Phe Asp Ser Arg Leu 290 295 300	14700

TCC GAG TCA CGC GCA GGC CTG GTG ATC AGT CCT CTT ATA GCC ATC CCC Ser Glu Ser Arg Ala Gly Leu Val Ile Ser Pro Leu Ile Ala Ile Pro 305 310 315	14748
AAA GTT TTG ATT ATA GTC GTT TCC GAC GGA GAC ATT TTG GGA TGG AGC Lys Val Leu Ile Ile Val Val Ser Asp Gly Asp Ile Leu Gly Trp Ser 320 325 330 335	14796
TAC ACG GTG CTC GGG AAA CGT AAC AGT CCG CGC GTA GTA GTC GAA ACG Tyr Thr Val Leu Gly Lys Arg Asn Ser Pro Arg Val Val Val Glu Thr 340 345 350	14844
CAC ATG CCC TCG AAG GTC CCG ATG AAC AAA GTA GTA ATT GGC AGT CCC His Met Pro Ser Lys Val Pro Met Asn Lys Val Val Ile Gly Ser Pro 355 360 365	14892
GGA CCA ATG GAC GAA ACG GGT AAC TAT AAA ATG TAC TTC GTC GTC GCG Gly Pro Met Asp Glu Thr Gly Asn Tyr Lys Met Tyr Phe Val Val Ala 370 375 380	14940
GGG GTG GCC GCG ACG TGC GTA ATT CTT ACA TGC GCT CTG CTT GTG GGG Gly Val Ala Ala Thr Cys Val Ile Leu Thr Cys Ala Leu Leu Val Gly 385 390 395	14988
AAA AAG AAG TGC CCC GCG CAC CAA ATG GGT ACT TTT TCC AAG ACC GAA Lys Lys Lys Cys Pro Ala His Gln Met Gly Thr Phe Ser Lys Thr Glu 400 405 410 415	15036
CCA TTG TAC GCG CCG CTC CCC AAA AAC GAG TTT GAG GCC GGC GGG CTT Pro Leu Tyr Ala Pro Leu Pro Lys Asn Glu Phe Glu Ala Gly Gly Leu 420 425 430	15084
ACG GAC GAT GAG GAA GTG ATT TAT GAC GAA GTA TAC GAA CCC CTA TTT Thr Asp Asp Glu Glu Val Ile Tyr Asp Glu Val Tyr Glu Pro Leu Phe 435 440 445	15132
CGC GGC TAC TGT AAG CAG GAA TTC CGC GAA GAT GTG AAT ACC TTT TTC Arg Gly Tyr Cys Lys Gln Glu Phe Arg Glu Asp Val Asn Thr Phe Phe 450 455 460	15180
GGT GCG GTC GTG GAG GGA GAA AGG GCC TTA AAC TTT AAA TCC GCC ATC Gly Ala Val Val Glu Gly Glu Arg Ala Leu Asn Phe Lys Ser Ala Ile 465 470 475	15228
GCA TCA ATG GCA GAT CGC ATC CTG GCA AAT AAA AGC GGC AGA AGG AAT Ala Ser Met Ala Asp Arg Ile Leu Ala Asn Lys Ser Gly Arg Arg Asn 480 485 490 495	15276
ATG GAT AGC TAT TAG TTGGTC ATG CCT TTT AAG ACC AGA GGG GCC GAA Met Asp Ser Tyr . Met Pro Phe Lys Thr Arg Gly Ala Glu 500 1 5	15324
GAC GCG GCC GCG GGC AAG AAC AGG TTT AAG AAA TCG AGA AAT CGG GAA Asp Ala Ala Ala Gly Lys Asn Arg Phe Lys Lys Ser Arg Asn Arg Glu 10 15 20 25	15372
ATC TTA CCG ACC AGA CTG CGT GGC ACC GGT AAG AAA ACT GCC GGA TTG Ile Leu Pro Thr Arg Leu Arg Gly Thr Gly Lys Lys Thr Ala Gly Leu 30 35 40	15420
TCC AAT TAT ACC CAG CCT ATT CCC TGG AAC CCT AAA TTC TGC AGC GCG Ser Asn Tyr Thr Gln Pro Ile Pro Trp Asn Pro Lys Phe Cys Ser Ala 45 50 55	15468
CGC GGG GAA TCT GAC AAC CAC GCG TGT AAA GAC ACT TTT TAT CGC AGG Arg Gly Glu Ser Asp Asn His Ala Cys Lys Asp Thr Phe Tyr Arg Arg 60 65 70	15516

ACG TGC TGC GCA TCG CGC TCT ACC GTT TCC AGT CAA CCC GAT TCC CCC Thr Cys Cys Ala Ser Arg Ser Thr Val Ser Ser Gln Pro Asp Ser Pro 75 80 85	15564
CAC ACA CCC ATG CCT ACT GAG TAT GGG CGC GTG CCC TCC GCA AAG CGC His Thr Pro Met Pro Thr Glu Tyr Gly Arg Val Pro Ser Ala Lys Arg 90 95 100 105	15612
AAA AAA CTA TCA TCT TCA GAC TGC GAG GGC GCG CAC CAA CCC CTA GTA Lys Lys Leu Ser Ser Ser Asp Cys Glu Gly Ala His Gln Pro Leu Val 110 115 120	15660
TCC TGT AAA CTT CCG GAT TCT CAA GCA GCA CCG GCG CGA ACC TAT AGT Ser Cys Lys Leu Pro Asp Ser Gln Ala Ala Pro Ala Arg Thr Tyr Ser 125 130 135	15708
TCT GCG CAA AGA TAT ACT GTT GAC GAG GTT TCG TCG CCA ACT CCG CCA Ser Ala Gln Arg Tyr Thr Val Asp Glu Val Ser Ser Pro Thr Pro Pro 140 145 150	15756
GGC GTC GAC GCT GTT GCG GAC TTA GAA ACG CGC GCG GAA CTT CCT GGC Gly Val Asp Ala Val Ala Asp Leu Glu Thr Arg Ala Glu Leu Pro Gly 155 160 165	15804
GCT ACG ACG GAA CAA ACG GAA AGT AAA AAT AAG CTC CCC AAC CAA CAA Ala Thr Thr Glu Gln Thr Glu Ser Lys Asn Lys Leu Pro Asn Gln Gln 170 175 180 185	15852
TCG CGC CTG AAG CCG AAA CCC ACA AAC GAG CAC GTC GGA GGG GAG CGG Ser Arg Leu Lys Pro Lys Pro Thr Asn Glu His Val Gly Gly Glu Arg 190 195 200	15900
TGC CCC TCC GAA GGC ACG GTC GAG GCG CCA TCG CTC GGC ATC CTC TCG Cys Pro Ser Glu Gly Thr Val Glu Ala Pro Ser Leu Gly Ile Leu Ser 205 210 215	15948
CGC GTC GGG GCA GCG ATA GCA AAC GAG CTG GCT CGT ATG CGG AGG GCG Arg Val Gly Ala Ala Ile Ala Asn Glu Leu Ala Arg Met Arg Arg Ala 220 225 230	15996
TGT CTT CCG CTC GCC GCG TCG GCG GCC GCT GCC GGA ATA GTG GCC TGG Cys Leu Pro Leu Ala Ala Ser Ala Ala Ala Ala Gly Ile Val Ala Trp 235 240 245	16044
GCC GCG GCG AGG GCC TTG CAG AAA CAA GGG CGG TAG CAGTAATAAT Ala Ala Ala Arg Ala Leu Gln Lys Gln Gly Arg 250 255 260	16090
AACCACACAA ATATTGACAA TAATAACGC GTACGCGG ATG AGT AAG TGT TAT Met Ser Lys Cys Tyr 1 5	16143
TGT CTC GCG CGC CAT CTT TAT AAA AGC CCG CGT TGC GTG GGC CGG CGG Cys Leu Ala Arg His Leu Tyr Lys Ser Pro Arg Cys Val Gly Arg Arg 10 15 20	16191
GTA GCA TTT GGA GGG TTG GCG ACC ATG TCG AGA CCT CCG ACG TCA CAT Val Ala Phe Gly Gly Leu Ala Thr Met Ser Arg Pro Pro Thr Ser His 25 30 35	16239
TTG GAC TTA GCT TTC TCG GCG GCC TTT AGG GGC ACG GAC CTG CCC GGA Leu Asp Leu Ala Phe Ser Ala Ala Phe Arg Gly Thr Asp Leu Pro Gly 40 45 50	16287
GGG AGA TTC TGG CGG GCG TCG CAG AGT TGC GAT ATT TTC TTT TGG CCC Gly Arg Phe Trp Arg Ala Ser Gln Ser Cys Asp Ile Phe Phe Trp Pro 55 60 65	16335

15564 15612 15660 15708 15756 15804 15852 15900 15948 15996 16044 16090 16143 16191 16239 16287 16335

GAT CTG GCC GCG GTG ATC GTA CAG GCC GCC CGC GCG TAT TTT GAA GGG Asp Leu Ala Ala Val Ile Val Gln Ala Ala Arg Ala Tyr Phe Glu Gly 70 75 80 85	16383
AAG GAA AGG CTG GGC AGT CTG CAG GTC GCC GAA GAT ATC ACG GCG CAC Lys Glu Arg Leu Gly Ser Leu Gln Val Ala Glu Asp Ile Thr Ala His 90 95 100	16431
GAC CCG CGA ATA GCG CCC GCG GCT AAG CGC GCC GTC GCA GCG GCG GTA Asp Pro Arg Ile Ala Pro Ala Ala Lys Arg Ala Val Ala Ala Val 105 110 115	16479
GGA CTG TGG ACC GCG CTG TCG GAG TTA GTT GGG GGG CCG AAC GGG GAG Gly Leu Trp Thr Ala Leu Ser Glu Leu Val Gly Gly Pro Asn Gly Glu 120 125 130	16527
TTG GAA AGC AAG GTC TGG GGC AAG CAG ATT CCC CGG GCC GCC GCG TGG Leu Glu Ser Lys Val Trp Gly Lys Gln Ile Pro Arg Ala Ala Trp 135 140 145	16575
GAA ATA AGA GAC GTG CCC AAA GTT CCA GTC ATT GGG CCG GAC ATT CTT Glu Ile Arg Asp Val Pro Lys Val Pro Val Ile Gly Pro Asp Ile Leu 150 155 160 165	16623
TCT TTT TTC TCC GCC GCC GTC GAG CTG CCG GTG CTC TAT ATC AGA GCC Ser Phe Phe Ser Ala Ala Val Glu Leu Pro Val Leu Tyr Ile Arg Ala 170 175 180	16671
CGG GGA GGG GCG CAC TCG CGG TCC GCG CAC TGG AAT AAC CAG AGC AGC Arg Gly Gly Ala His Ser Arg Ser Ala His Trp Asn Asn Gln Ser Ser 185 190 195	16719
GCG CCG GCC GCC GGA CTC GCG GCG ATA AGG ATA GGC ATG GAG ATG GTG Ala Pro Ala Ala Gly Leu Ala Ala Ile Arg Ile Gly Met Glu Met Val 200 205 210	16767
CGG AGC CTC CTG GTG ATA GCG CTG CCT CTG TCA AAC TTC ACC CTC CCG Arg Ser Leu Leu Val Ile Ala Leu Pro Leu Ser Asn Phe Thr Leu Pro 215 220 225	16815
GAA GAC CTC CCC GAA GGT TCC CAA AAC TCG ATC CGC GCG TTC GTG GCC Glu Asp Leu Pro Glu Gly Ser Gln Asn Ser Ile Arg Ala Phe Val Ala 230 235 240 245	16863
CAC CTC ATG AAC TGT GTA GCT ACC GAT AAG ATC ATG TCT CCG GAC GTG His Leu Met Asn Cys Val Ala Thr Asp Lys Ile Met Ser Pro Asp Val 250 255 260	16911
CGC GTC CCA GTC GAA GAA AGC TTT TAC AGC CAC TGT TTA AGG GAA ATC Arg Val Pro Val Glu Glu Ser Phe Tyr Ser His Cys Leu Arg Glu Ile 265 270 275	16959
ATT ATG TGC GAG AGA GCT TTT TGT TAC CCG TGC AAT CCC CCG CCA AAA Ile Met Cys Glu Arg Ala Phe Cys Tyr Pro Cys Asn Pro Pro Pro Lys 280 285 290	17007
TGG TGA GCTCAGGGTC CCATTTACCC CCGCAACACC CTCTCGCCGC CAGGGCGCGC Trp 295	17063
GCTCTATCTT TCTCTATGTC CCGTCGCCAC CGGCCTAACC GAACGGTGGA ACGGGGCCGC	17123
CCGGGAAAGC CTAGCTCCGC ACAGACACAG ACAGACAAAC GGCCTCTCGA TTGCAACAAC	17183
GTGAAAAACA CACAATAATA TTA CTTTATT TATTTTCGCAG CGCTCGCGTG TCGCTCGTTT	17243
CTGGGGGGGG GGGGGGGTTG TGTTTCGCTG CCGCGGAGTG GGTGAGGGGG GAGAGTGGAC	17303

GGAGGACAGT GTAAAAACCC GCGAGGTTGT CAGGGACGCG GAGGTAAGGA AGCCGCTAGA	17363
GGGCGTCATT CTCCCGTCAA CGGCGCCGCG CCAGCGCCAG CGCGATTCCA GCGTCCCTCG	17423
CAAAGATCGA GGCCTCACT TCGGGAGAGT TGGCGGCAGC CGCGCCGGCG CGCAAGGCGG	17483
CCAGGTATTC GCGACGGCGC ATCTCCGATT GCGGGACTCT CCCCCTCCCG ACGCAGAAAA	17543
GA CTCTGCAC GTAAATCGAG TCGTACAAAC ACGCTTCGCG GCACGGCCGA GGGTGCCACA	17603
AGCAGCACCA GTGCCCCGCC GCCAGGAGAG ACCGGGAGGT CTCTCGCTCG GCGGACGCGA	17663
GGTCGGCCGG CAGGTGTCTGG GACAGCCAGG ATAACAGTTC TTTCTCGATC ACGAAACGCA	17723
TATTCTCGCT CTGCATGGTA CGGCTCTCGT CCTCGAAGCG GTCACCGTCC AGAGAGTCGA	17783
GCCAGAAATC GCCCTCGATC CCTTCCATTG CCTCCTCTAA TTCTCCCAAC CCGTTGCCGT	17843
TATTCGGGTC AGTGGGGGAG TTGGCGACGC TCTCCGTCGA CGCCCACCGC GGCCTCAAAC	17903
CTAGGCCGCG CGTCGCCCGG CTGGCCCCCA GAAAAGCCGA ACGTAGCCGT TCGTTGGCAG	17963
CAATCAGCGC GTTGCGGCGG TCTCTCGCTG ACGTGAATC TCCGTAACCG TCCTTGAGTT	18023
CGGACGATAT CTCGACTAAC TCGCGCCAGA GCCGCGAGGC GATCCGAATG CACGGGTCTA	18083
CCGAGTCGGC CGACTCCGAC GAGGCGACAG CGGCACCTTG CCGCCTGCGC TCGCCACGAG	18143
GTACCGCGTG CGCAGTAATG TGATCGCTGT CCATCAGCGC CAGCGGGTAG CACCCGTCGA	18203
GCATGTTTTT CATTAGGGA TGTGTCTAGA GGAGAGCGGT CCGGGCGGTC TACTGCGGTT	18263
GTGCTGGGCC GAGTTGGACG GCTACGGATT GCGCCGGGCG TGAAGGGGGG GGGGCGGCGG	18323
GATGTCCGGC GGTCGCAAAG GGGCGCGCGT CCGCTTCTGC GTGAAGGCTG AGCGGGAAAG	18383
AAGTTCTGGA TGAGAATGGA TCGAGCGGGC AATAAATGTC CAGAGTAGGG GGGTGGGAGG	18443
GAGGGGGAGG TTCTGCCCCG CGTCTCCTCT ATCTGCTCGT CGAGGCCTCG GCCTTGCGTC	18503
GCCGTGCAGG GGTCGAGGCC GCTTCTTCTT TTTTACTTCT CTCCTCGGAT TCCTCGTCAG	18563
AGGAAGAAGA AAATGACAAC CTCCGTCTTT TAAGAGTGCG CCTACCCGCC CTGGCGGCCG	18623
AAGCCTTCCG TGGGTCTTTG CGGGTGCCGC GCACCGCAAT AACGCACGGA CGCGGGGGAT	18683
AGCAAATGGC GCGGCGCCG GAGAGCTGTC GTCAATAAAG TCTAAGTCAG ATTGCGTGGG	18743
CTCTGACTCG GTGGAGCTGT GTCCCGTGTC CTCCTCGCCC AAGTCCACTC CCCGGCACCC	18803
AGGCTGCTCT TCCTCCGACT CCGGGTCGCT CCAGCTCCTC CCGCGTGCCG GTTCTTCGTC	18863
CTCCGATACG TCCGAAAAGA AAAACTTCTG GGAGAGCTCT TCGGGATCC	18912

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Met Glu Asn Met Leu Asp Gly Cys Tyr Pro Leu Ala Leu Met Asp Ser
1 5 10 15
Asp His Ile Thr Ala His Ala Val Pro Arg Gly Glu Arg Arg Arg Gln
20 25 30
Gly Ala Ala Val Ala Ser Ser Glu Ser Ala Asp Ser Val Asp Pro Cys
35 40 45
Ile Arg Ile Ala Ser Arg Leu Trp Arg Glu Leu Val Glu Ile Ser Ser
50 55 60
Glu Leu Lys Asp Gly Tyr Gly Glu Phe Thr Ser Ala Arg Asp Arg Arg
65 70 75 80
Asn Ala Leu Ile Ala Ala Asn Glu Arg Leu Arg Ser Ala Phe Leu Gly
85 90 95
Ala Ser Arg Ala Thr Arg Gly Leu Gly Leu Arg Pro Arg Trp Ala Ser
100 105 110
Thr Glu Ser Val Ala Asn Ser Pro Thr Asp Pro Asn Asn Gly Asn Gly
115 120 125
Leu Gly Glu Leu Glu Glu Ala Met Glu Gly Ile Glu Gly Asp Phe Trp
130 135 140
Leu Asp Ser Leu Asp Gly Asp Arg Phe Glu Asp Glu Ser Arg Thr Met
145 150 155 160
Gln Ser Glu Asn Met Arg Phe Val Ile Glu Lys Glu Leu Leu Ser Trp
165 170 175
Leu Ser Arg His Leu Pro Ala Asp Leu Ala Ser Ala Glu Arg Glu Thr
180 185 190
Ser Arg Ser Leu Leu Ala Ala Gly His Trp Cys Cys Leu Trp His Pro
195 200 205
Arg Pro Cys Arg Glu Ala Cys Leu Tyr Asp Ser Ile Tyr Val Gln Ser
210 215 220
Leu Phe Cys Val Gly Thr Gly Arg Val Pro Gln Ser Glu Met Arg Arg
225 230 235 240
Arg Glu Tyr Leu Ala Ala Leu Arg Ala Gly Ala Ala Ala Ala Asn Ser
245 250 255
Pro Glu Val Ser Ala Ser Ile Phe Ala Arg Asp Ala Gly Ile Ala Leu
260 265 270
Ala Leu Ala Arg Arg Arg .
275

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Met Ser Lys Cys Tyr Cys Leu Ala Arg His Leu Tyr Lys Ser Pro Arg
1 5 10 15
Cys Val Gly Arg Arg Val Ala Phe Gly Gly Leu Ala Thr Met Ser Arg
20 25 30
Pro Pro Thr Ser His Leu Asp Leu Ala Phe Ser Ala Ala Phe Arg Gly
35 40 45
Thr Asp Leu Pro Gly Gly Arg Phe Trp Arg Ala Ser Gln Ser Cys Asp
50 55 60
Ile Phe Phe Trp Pro Asp Leu Ala Ala Val Ile Val Gln Ala Ala Arg
65 70 75 80
Ala Tyr Phe Glu Gly Lys Glu Arg Leu Gly Ser Leu Gln Val Ala Glu
85 90 95
Asp Ile Thr Ala His Asp Pro Arg Ile Ala Pro Ala Ala Lys Arg Ala
100 105 110
Val Ala Ala Ala Val Gly Leu Trp Thr Ala Leu Ser Glu Leu Val Gly
115 120 125
Gly Pro Asn Gly Glu Leu Glu Ser Lys Val Trp Gly Lys Gln Ile Pro
130 135 140
Arg Ala Ala Ala Trp Glu Ile Arg Asp Val Pro Lys Val Pro Val Ile
145 150 155 160
Gly Pro Asp Ile Leu Ser Phe Phe Ser Ala Ala Val Glu Leu Pro Val
165 170 175
Leu Tyr Ile Arg Ala Arg Gly Gly Ala His Ser Arg Ser Ala His Trp
180 185 190
Asn Asn Gln Ser Ser Ala Pro Ala Ala Gly Leu Ala Ala Ile Arg Ile
195 200 205
Gly Met Glu Met Val Arg Ser Leu Leu Val Ile Ala Leu Pro Leu Ser
210 215 220
Asn Phe Thr Leu Pro Glu Asp Leu Pro Glu Gly Ser Gln Asn Ser Ile
225 230 235 240
Arg Ala Phe Val Ala His Leu Met Asn Cys Val Ala Thr Asp Lys Ile
245 250 255
Met Ser Pro Asp Val Arg Val Pro Val Glu Glu Ser Phe Tyr Ser His
260 265 270
Cys Leu Arg Glu Ile Ile Met Cys Glu Arg Ala Phe Cys Tyr Pro Cys
275 280 285
Asn Pro Pro Pro Lys Trp .
290

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 229 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Met Ala Pro Val Lys Val Thr Ile Val Ser Ala Val Asp Ser His Tyr
1 5 10 15
Lys Leu Pro Asn Ser Arg Phe Glu Leu Ser Asp Ser Gly Trp Lys Glu
20 25 30
Leu Val His Ala Val Lys Thr Met Ala Ser Tyr Asp Arg Pro Ser Thr
35 40 45
Leu Ser Val Ile Val Arg Pro Ala Ser Leu Tyr Glu Val Ser Gly Glu
50 55 60
Leu Phe Ser Leu Pro Arg Met Cys Arg Pro Val Ile Arg Phe Gly Glu
65 70 75 80
Gly Gly Asp Pro Pro Gly Val Ser Pro Glu Trp Ser Gly Leu Asp Ala
85 90 95
Gly Phe Tyr His Leu Ser Ser Gly Ala Tyr Ala Ala Lys Glu Phe His
100 105 110
Leu Trp Val Leu Gly Thr Ala Asp Ile Cys Met Ala Ala Leu Asn Leu
115 120 125
Pro Ala Pro Lys Thr Phe Leu Ile Thr Glu Thr Gly Gly Lys Asn Phe
130 135 140
Glu Arg Gly Val Glu Ile Phe Leu Val Asn Gly Asp Lys Thr Thr Leu
145 150 155 160
Ser Leu Ser His Pro Ser Val Trp Thr Thr Leu Ala Pro Ser Ser Leu
165 170 175
Arg Thr Pro Trp Pro Tyr Ser Thr Val Lys Phe Leu Lys Val Lys Pro
180 185 190
Asn Ser Ala Ala Tyr Cys Val Ser Asp Ser Asp Asp Gly Glu Arg Gln
195 200 205
Pro Lys Phe Phe Leu Gly Ser Leu Phe Lys Ser Lys Lys Pro Arg Ser
210 215 220
Pro Arg Arg Arg Arg
225

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Met Arg Phe Arg Arg Ile Cys Ser Arg Ser Arg Ala Glu Lys Arg Arg
1 5 10 15
Arg Thr Thr Glu Asn Pro Leu Thr Ser Lys Arg Val Cys Val Leu Asp
20 25 30
Ser Phe Ser Arg Thr Met Ser Leu Arg Pro Tyr Ala Glu Ile Leu Pro
35 40 45

Thr Ala Glu Gly Val Glu Arg Leu Ala Glu Leu Val Ser Val Thr Met
50 55 60

Thr Glu Arg Ala Glu Pro Val Thr Glu Asn Thr Ala Val Asn Ser Ile
65 70 75 80

Pro Pro Ala Asn Glu Asn Gly Gln Asn Phe Ala Tyr Ala Gly Asp Gly
85 90 95

Pro Ser Thr Thr Glu Lys Val Asp Gly Ser His Thr Asp Phe Asp Glu
100 105 110

Ala Ser Ser Asp Tyr Ala Gly Pro Val Pro Leu Ala Gln Thr Arg Leu
115 120 125

Lys His Ser Asp Glu Phe Leu Gln His Phe Arg Val Leu Asp Asp Leu
130 135 140

Val Glu Gly Ala Tyr Gly Phe Ile Cys Asp Val Arg Arg Tyr Thr Glu
145 150 155 160

Glu Glu Gln Arg Arg Arg Gly Val Asn Ser Thr Asn Gln Gly Lys Ser
165 170 175

Lys Cys Lys Arg Leu Ile Ala Lys Tyr Val Lys Asn Gly Thr Arg Ala
180 185 190

Ala Ser Gln Leu Glu Asn Glu Ile Leu Val Leu Gly Arg Leu Asn His
195 200 205

Glu Asn Val Leu Lys Ile Gln Glu Ile Leu Arg Tyr Pro Asp Asn Thr
210 215 220

Tyr Met Leu Thr Gln Arg Tyr Gln Phe Asp Leu Tyr Ser Tyr Met Tyr
225 230 235 240

Asp Glu Ala Phe Asp Trp Lys Asp Ser Pro Met Leu Lys Gln Thr Arg
245 250 255

Arg Ile Met Lys Gln Leu Met Ser Ala Val Ser Tyr Ile His Ser Lys
260 265 270

Lys Leu Ile His Arg Asp Ile Lys Leu Glu Asn Ile Phe Leu Asn Cys
275 280 285

Asp Gly Lys Thr Val Leu Gly Asp Phe Gly Thr Val Thr Pro Phe Glu
290 295 300

Asn Glu Arg Glu Pro Phe Glu Tyr Gly Trp Val Gly Thr Val Ala Thr
305 310 315 320

Asn Ser Pro Glu Ile Leu Ala Arg Asp Ser Tyr Cys Glu Ile Thr Asp
325 330 335

Ile Trp Ser Cys Gly Val Val Leu Leu Glu Met Val Ser His Glu Phe
340 345 350

Cys Pro Ile Gly Asp Gly Gly Gly Asn Pro His Gln Gln Leu Leu Lys
355 360 365

Val Ile Asp Ser Leu Ser Val Cys Asp Glu Glu Phe Pro Asp Pro Pro
370 375 380

Cys Asn Leu Tyr Asn Tyr Leu His Tyr Ala Ser Ile Asp Arg Ala Gly
385 390 395 400

His Thr Val Pro Ser Leu Ile Arg Asn Leu His Leu Pro Ala Asp Val
405 410 415
Glu Tyr Pro Leu Val Lys Met Leu Thr Phe Asp Trp Arg Leu Arg Pro
420 425 430
Ser Ala Ala Glu Val Leu Ala Met Pro Leu Phe Ser Ala Glu Glu Glu
435 440 445
Arg Thr Ile Thr Ile Ile His Gly Lys His Lys Pro Ile Arg Pro Glu
450 455 460
Ile Arg Ala Arg Val Pro Arg Ser Met Ser Glu Gly
465 470 475

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 623 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Met Thr Leu Pro His Arg Leu Thr Lys Arg Pro Phe Ala Arg Arg Phe
1 5 10 15
Cys Ser Val Phe Val Ile His Tyr Ser Glu Thr Lys Leu Asp Arg Tyr
20 25 30
Asn Lys Thr Met Leu Leu Tyr Arg Pro Asp Ser Thr Met Arg His Ser
35 40 45
Gly Gly Asp Ala Asn His Arg Gly Ile Arg Pro Arg Arg Lys Ser Ile
50 55 60
Gly Ala Phe Ser Ala Arg Glu Lys Thr Gly Lys Arg Asn Ala Leu Thr
65 70 75 80
Glu Ser Ser Ser Ser Ser Asp Met Leu Asp Pro Phe Ser Thr Asp Lys
85 90 95
Glu Phe Gly Gly Lys Trp Thr Val Asp Gly Pro Ala Asp Ile Thr Ala
100 105 110
Glu Val Leu Ser Gln Ala Trp Asp Val Leu Gln Leu Val Lys His Glu
115 120 125
Asp Ala Glu Glu Glu Arg Val Thr Tyr Glu Ser Lys Pro Thr Pro Ile
130 135 140
Gln Pro Phe Asn Ala Trp Pro Asp Gly Pro Ser Trp Asn Ala Gln Asp
145 150 155 160
Phe Thr Arg Ala Pro Ile Val Tyr Pro Ser Ala Glu Val Leu Asp Ala
165 170 175
Glu Ala Leu Lys Val Gly Ala Phe Val Ser Arg Val Leu Gln Cys Val
180 185 190
Pro Phe Thr Arg Ser Lys Lys Ser Val Thr Val Arg Asp Ala Gln Ser
195 200 205

Phe Leu Gly Asp Ser Phe Trp Arg Ile Met Gln Asn Val Tyr Thr Val
 210 215 220
 Val Leu Arg Gln His Ile Thr Arg Leu Arg His Pro Ser Ser Lys Ser
 225 230 235 240
 Ile Val Asn Cys Asn Asp Pro Leu Trp Tyr Ala Tyr Ala Asn Gln Phe
 245 250 255
 His Trp Arg Gly Met Arg Val Pro Ser Leu Lys Leu Ala Ser Pro Pro
 260 265 270
 Glu Glu Asn Ile Gln His Gly Pro Met Ala Ala Val Phe Arg Asn Ala
 275 280 285
 Gly Ala Gly Leu Phe Leu Trp Pro Ala Met Arg Ala Ala Phe Glu Glu
 290 295 300
 Arg Asp Lys Arg Leu Leu Arg Ala Cys Leu Ser Ser Leu Asp Ile Met
 305 310 315 320
 Asp Ala Ala Val Leu Ala Ser Phe Pro Phe Tyr Trp Arg Gly Val Gln
 325 330 335
 Asp Thr Ser Arg Phe Glu Pro Ala Leu Gly Cys Leu Ser Glu Tyr Phe
 340 345 350
 Ala Leu Val Val Leu Leu Ala Glu Thr Val Leu Ala Thr Met Phe Asp
 355 360 365
 His Ala Leu Val Phe Met Arg Ala Leu Ala Asp Gly Asn Phe Asp Asp
 370 375 380
 Tyr Asp Glu Thr Arg Tyr Ile Asp Pro Val Lys Asn Glu Tyr Leu Asn
 385 390 395 400
 Gly Ala Glu Gly Thr Leu Leu Arg Gly Ile Val Ala Ser Asn Thr Ala
 405 410 415
 Leu Ala Val Val Cys Ala Asn Thr Tyr Ser Thr Ile Arg Lys Leu Pro
 420 425 430
 Ser Val Ala Thr Ser Ala Cys Asn Val Ala Tyr Arg Thr Glu Thr Leu
 435 440 445
 Lys Ala Arg Arg Pro Gly Met Ser Asp Ile Tyr Arg Ile Leu Gln Lys
 450 455 460
 Glu Phe Phe Phe Tyr Ile Ala Trp Leu Gln Arg Val Ala Thr His Ala
 465 470 475 480
 Asn Phe Cys Leu Asn Ile Leu Lys Arg Ser Val Asp Thr Gly Ala Pro
 485 490 495
 Pro Phe Leu Phe Arg Ala Ser Ser Glu Lys Arg Leu Gln Gln Leu Asn
 500 505 510
 Lys Met Leu Cys Pro Leu Leu Val Pro Ile Gln Tyr Glu Asp Phe Ser
 515 520 525
 Lys Ala Met Gly Ser Glu Leu Lys Arg Glu Lys Leu Glu Thr Phe Val
 530 535 540
 Lys Ala Ile Ser Ser Asp Arg Asp Pro Arg Gly Ser Leu Arg Phe Leu
 545 550 555 560

Ile Ser Asp His Ala Arg Glu Ile Ile Ala Asp Gly Val Arg Phe Lys
565 570 575
Pro Val Ile Asp Glu Pro Val Arg Ala Ser Val Ala Leu Ser Thr Ala
580 585 590
Ala Ala Gly Lys Val Lys Ala Arg Arg Leu Thr Ser Val Arg Ala Pro
595 600 605
Val Pro Gly Ala Gly Ala Val Ser Ala Arg Arg Lys Ser Glu Ile
610 615 620

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 292 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Met Ser Gly Phe Ser Asn Ile Gly Ser Ile Ala Thr Val Ser Leu Val
1 5 10 15
Cys Ser Leu Leu Cys Ala Ser Val Leu Gly Ala Pro Val Leu Asp Gly
20 25 30
Leu Glu Ser Ser Pro Phe Pro Phe Gly Gly Lys Ile Ile Ala Gln Ala
35 40 45
Cys Asn Arg Thr Thr Ile Glu Val Thr Val Pro Trp Ser Asp Tyr Ser
50 55 60
Gly Arg Thr Glu Gly Val Ser Val Glu Val Lys Trp Phe Tyr Gly Asn
65 70 75 80
Ser Asn Pro Glu Ser Phe Val Phe Gly Val Asp Ser Glu Thr Gly Ser
85 90 95
Gly His Glu Asp Leu Ser Thr Cys Trp Ala Leu Ile His Asn Leu Asn
100 105 110
Ala Ser Val Cys Arg Ala Ser Asp Ala Gly Ile Pro Asp Phe Asp Lys
115 120 125
Gln Cys Glu Lys Val Gln Arg Arg Leu Arg Ser Gly Val Glu Leu Gly
130 135 140
Ser Tyr Val Ser Gly Asn Gly Ser Leu Val Leu Tyr Pro Gly Met Tyr
145 150 155 160
Asp Ala Gly Ile Tyr Ala Tyr Gln Leu Ser Val Gly Gly Lys Gly Tyr
165 170 175
Thr Gly Ser Val Tyr Leu Asp Val Gly Pro Asn Pro Gly Cys His Asp
180 185 190
Gln Tyr Gly Tyr Thr Tyr Tyr Ser Leu Ala Asp Glu Ala Ser Asp Leu
195 200 205
Ser Ser Tyr Asp Val Ala Ser Pro Glu Leu Asp Gly Pro Met Glu Glu
210 215 220

Asp Tyr Ser Asn Cys Leu Asp Met Pro Pro Leu Arg Pro Trp Thr Thr
225 230 235 240
Val Cys Ser His Asp Val Glu Glu Gln Glu Asn Ala Thr Asp Glu Leu
245 250 255
Tyr Leu Trp Asp Glu Glu Cys Ala Gly Pro Leu Asp Glu Tyr Val Asp
260 265 270
Glu Arg Ser Glu Thr Met Pro Arg Met Val Val Phe Ser Pro Pro Ser
275 280 285
Thr Leu Gln Gln
290

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 985 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Met Gly Thr Met Leu Val Leu Arg Leu Phe Leu Leu Ala Val Ala Asp
1 5 10 15
Ala Ala Leu Pro Thr Gly Arg Phe Cys Arg Val Trp Lys Val Pro Pro
20 25 30
Gly Gly Thr Ile Gln Glu Asn Leu Ala Val Leu Ala Glu Ser Pro Val
35 40 45
Thr Gly His Ala Thr Tyr Pro Pro Pro Glu Gly Ala Val Ser Phe Gln
50 55 60
Ile Phe Ala Asp Thr Pro Thr Leu Arg Ile Arg Tyr Gly Ala Thr Glu
65 70 75 80
Asp Glu Leu Ala Leu Glu Arg Gly Thr Ser Ala Ser Asp Ala Asp Asn
85 90 95
Val Thr Phe Ser Leu Ser Tyr Arg Pro Arg Pro Glu Ile His Gly Ala
100 105 110
Tyr Phe Thr Ile Gly Val Phe Ala Thr Gly Gln Ser Thr Glu Ser Ser
115 120 125
Tyr Ser Val Ile Ser Arg Val Leu Val Asn Ala Ser Leu Glu Arg Ser
130 135 140
Val Arg Leu Glu Thr Pro Cys Asp Glu Asn Phe Leu Gln Asn Glu Pro
145 150 155 160
Thr Trp Gly Ser Lys Arg Trp Leu Gly Pro Pro Ser Pro Tyr Val Arg
165 170 175
Asp Asn Asp Val Ala Val Leu Thr Lys Ala Gln Tyr Ile Gly Glu Cys
180 185 190
Tyr Ser Asn Ser Ala Ala Gln Thr Gly Leu Thr Ser Leu Asn Met Thr
195 200 205

Phe 210	Phe	Tyr	Ser	Pro	Lys	Arg 215	Ile	Val	Asn	Val	Thr 220	Trp	Thr	Thr	Gly
Gly 225	Pro	Ser	Pro	Ser	Arg 230	Ile	Thr	Val	Tyr	Ser 235	Ser	Arg	Glu	Asn	Gly 240
Gln	Pro	Val	Leu	Arg 245	Asn	Val	Ser	Asp	Gly 250	Phe	Leu	Val	Lys	Tyr 255	Thr
Pro	Asp	Ile	Asp 260	Gly	Arg	Ala	Met	Ile 265	Asn	Val	Ile	Ala	Asn 270	Tyr	Ser
Pro	Ala	Asp 275	Ser	Gly	Ser	Val	Leu 280	Ala	Phe	Thr	Ala	Phe 285	Arg	Glu	Gly
Lys	Leu 290	Pro	Ser	Ala	Ile	Gln 295	Leu	His	Arg	Ile	Asp 300	Met	Ser	Gly	Thr
Glu 305	Pro	Pro	Gly	Thr	Glu 310	Thr	Thr	Phe	Asp	Cys 315	Gln	Lys	Met	Ile	Glu 320
Thr	Pro	Tyr	Arg	Ala 325	Leu	Gly	Ser	Asn	Val 330	Pro	Arg	Asp	Asp	Ser 335	Ile
Arg	Pro	Gly	Ala 340	Thr	Leu	Pro	Pro	Phe 345	Asp	Thr	Ala	Ala	Pro 350	Asp	Phe
Asp	Thr	Gly 355	Thr	Ser	Pro	Thr	Pro 360	Thr	Thr	Val	Pro	Glu 365	Pro	Ala	Ile
Thr	Thr 370	Leu	Ile	Pro	Arg	Ser 375	Thr	Ser	Asp	Met	Gly 380	Phe	Phe	Ser	Thr
Ala 385	Arg	Ala	Thr	Gly	Ser 390	Glu	Thr	Leu	Ser	Val 395	Pro	Val	Gln	Glu	Thr 400
Asp	Arg	Thr	Leu	Ser 405	Thr	Thr	Pro	Leu	Thr 410	Leu	Pro	Leu	Thr	Pro 415	Gly
Glu	Ser	Glu	Asn 420	Thr	Leu	Phe	Pro	Thr 425	Thr	Ala	Pro	Gly	Ile 430	Ser	Thr
Glu	Thr 435	Pro	Ser	Ala	Ala	His	Glu 440	Thr	Thr	Gln	Thr	Gln 445	Ser	Ala	Glu
Thr	Val 450	Val	Phe	Thr	Gln	Ser 455	Pro	Ser	Thr	Glu	Ser 460	Glu	Thr	Ala	Arg
Ser 465	Gln	Ser	Gln	Glu	Pro 470	Trp	Tyr	Phe	Thr	Gln 475	Thr	Pro	Ser	Thr	Glu 480
Gln	Ala	Ala	Leu	Thr 485	Gln	Thr	Gln	Ile	Ala 490	Glu	Thr	Glu	Ala	Leu 495	Phe
Thr	Gln	Thr	Pro 500	Ser	Ala	Glu	Gln	Met 505	Thr	Phe	Thr	Gln	Thr 510	Pro	Gly
Ala	Glu	Thr 515	Glu	Ala	Pro	Ala	Gln 520	Thr	Pro	Ser	Thr	Ile 525	Pro	Glu	Ile
Phe	Thr 530	Gln	Ser	Arg	Ser	Thr 535	Pro	Pro	Glu	Thr	Ala 540	Arg	Ala	Pro	Ser
Ala 545	Ala	Pro	Glu	Val	Phe 550	Thr	Gln	Ser	Ser	Ser 555	Thr	Val	Thr	Glu	Val 560

Phe Thr Gln Thr Pro Ser Thr Val Pro Lys Thr Thr Leu Ser Ser Ser
 565 570 575
 Thr Glu Pro Ala Ile Phe Thr Arg Thr Gln Ser Ala Gly Thr Glu Ala
 580 585 590
 Phe Thr Gln Thr Ser Ser Ala Glu Pro Asp Thr Met Arg Thr Gln Ser
 595 600 605
 Thr Glu Thr His Phe Phe Thr Gln Ala Pro Ser Thr Val Pro Lys Ala
 610 615 620
 Thr Gln Thr Pro Ser Thr Glu Pro Glu Val Leu Thr Gln Ser Pro Ser
 625 630 635 640
 Thr Glu Pro Val Pro Phe Thr Arg Thr Leu Gly Ala Glu Pro Glu Ile
 645 650 655
 Thr Gln Thr Pro Ser Ala Ala Pro Glu Val Tyr Thr Arg Ser Ser Ser
 660 665 670
 Thr Met Pro Glu Thr Ala Gln Ser Thr Pro Leu Ala Ser Gln Asn Pro
 675 680 685
 Thr Ser Ser Gly Thr Gly Thr His Asn Thr Glu Pro Arg Thr Tyr Pro
 690 695 700
 Val Gln Thr Thr Pro His Thr Gln Lys Leu Tyr Thr Glu Asn Lys Thr
 705 710 715 720
 Leu Ser Phe Pro Thr Val Val Ser Glu Phe His Glu Met Ser Thr Ala
 725 730 735
 Glu Ser Gln Thr Pro Leu Leu Asp Val Lys Ile Val Glu Val Lys Phe
 740 745 750
 Ser Asn Asp Gly Glu Val Thr Ala Thr Cys Val Ser Thr Val Lys Ser
 755 760 765
 Pro Tyr Arg Val Glu Thr Asn Trp Lys Val Asp Leu Val Asp Val Met
 770 775 780
 Asp Glu Ile Ser Gly Asn Ser Pro Ala Gly Val Phe Asn Ser Asn Glu
 785 790 795 800
 Lys Trp Gln Lys Gln Leu Tyr Tyr Arg Val Thr Asp Gly Arg Thr Ser
 805 810 815
 Val Gln Leu Met Cys Leu Ser Cys Thr Ser His Ser Pro Glu Pro Tyr
 820 825 830
 Cys Leu Phe Asp Thr Ser Leu Ile Ala Arg Glu Lys Asp Ile Ala Pro
 835 840 845
 Glu Leu Tyr Phe Thr Ser Asp Pro Gln Thr Ala Tyr Cys Thr Ile Thr
 850 855 860
 Leu Pro Ser Gly Val Val Pro Arg Phe Glu Trp Ser Leu Asn Asn Val
 865 870 875 880
 Ser Leu Pro Glu Tyr Leu Thr Ala Thr Thr Val Val Ser His Thr Ala
 885 890 895
 Gly Gln Ser Thr Val Trp Lys Ser Ser Ala Arg Ala Gly Glu Ala Trp
 900 905 910

Ile Ser Gly Arg Gly Gly Asn Ile Tyr Glu Cys Thr Val Leu Ile Ser
915 920 925
Asp Gly Thr Arg Val Thr Thr Arg Lys Glu Arg Cys Leu Thr Asn Thr
930 935 940
Trp Ile Ala Val Glu Asn Gly Ala Ala Gln Ala Gln Leu Tyr Ser Leu
945 950 955 960
Phe Ser Gly Leu Val Ser Gly Leu Cys Gly Ser Ile Ser Ala Leu Tyr
965 970 975
Ala Thr Leu Trp Thr Ala Ile Tyr Phe
980 985

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Met His Arg Pro His Leu Arg Arg His Ser Arg Tyr Tyr Ala Lys Gly
1 5 10 15
Glu Val Leu Asn Lys His Met Asp Cys Gly Gly Lys Arg Cys Cys Ser
20 25 30
Gly Ala Ala Val Phe Thr Leu Phe Trp Thr Cys Val Arg Ile Met Arg
35 40 45
Glu His Ile Cys Phe Val Arg Asn Ala Met Asp Arg His Leu Phe Leu
50 55 60
Arg Asn Ala Phe Trp Thr Ile Val Leu Leu Ser Ser Phe Ala Ser Gln
65 70 75 80
Ser Thr Ala Ala Val Thr Tyr Asp Tyr Ile Leu Gly Arg Arg Ala Leu
85 90 95
Asp Ala Leu Thr Ile Pro Ala Val Gly Pro Tyr Asn Arg Tyr Leu Thr
100 105 110
Arg Val Ser Arg Gly Cys Asp Val Val Glu Leu Asn Pro Ile Ser Asn
115 120 125
Val Asp Asp Met Ile Ser Ala Ala Lys Glu Lys Glu Lys Gly Gly Pro
130 135 140
Phe Glu Ala Ser Val Val Trp Phe Tyr Val Ile Lys Gly Asp Asp Gly
145 150 155 160
Glu Asp Lys Tyr Cys Pro Ile Tyr Arg Lys Glu Tyr Arg Glu Cys Gly
165 170 175
Asp Val Gln Leu Leu Ser Glu Cys Ala Val Gln Ser Ala Gln Met Trp
180 185 190
Ala Val Asp Tyr Val Pro Ser Thr Leu Val Ser Arg Asn Gly Ala Gly
195 200 205

Leu Thr Ile Phe Ser Pro Thr Ala Ala Leu Ser Gly Gln Tyr Leu Leu
210 215 220

Thr Leu Lys Ile Gly Arg Phe Ala Gln Thr Ala Leu Val Thr Leu Glu
225 230 235 240

Val Asn Asp Arg Cys Leu Lys Ile Gly Ser Gln Leu Asn Phe Leu Pro
245 250 255

Ser Lys Cys Trp Thr Thr Glu Gln Tyr Gln Thr Gly Phe Gln Gly Glu
260 265 270

His Leu Tyr Pro Ile Ala Asp Thr Asn Thr Arg His Ala Asp Asp Val
275 280 285

Tyr Arg Gly Tyr Glu Asp Ile Leu Gln Arg Trp Asn Asn Leu Leu Arg
290 295 300

Lys Lys Asn Pro Ser Ala Pro Asp Pro Arg Pro Asp Ser Val Pro Gln
305 310 315 320

Glu Ile Pro Ala Val Thr Lys Lys Ala Glu Gly Arg Thr Pro Asp Ala
325 330 335

Glu Ser Ser Glu Lys Lys Ala Pro Pro Glu Asp Ser Glu Asp Asp Met
340 345 350

Gln Ala Glu Ala Ser Gly Glu Asn Pro Ala Ala Leu Pro Glu Asp Asp
355 360 365

Glu Val Pro Glu Asp Thr Glu His Asp Asp Pro Asn Ser Asp Pro Asp
370 375 380

Tyr Tyr Asn Asp Met Pro Ala Val Ile Pro Val Glu Glu Thr Thr Lys
385 390 395 400

Ser Ser Asn Ala Val Ser Met Pro Ile Phe Ala Ala Phe Val Ala Cys
405 410 415

Ala Val Ala Leu Val Gly Leu Leu Val Trp Ser Ile Val Lys Cys Ala
420 425 430

Arg Ser .

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Met Ala Ser Leu Leu Gly Thr Leu Ala Leu Leu Ala Ala Thr Leu Ala
1 5 10 15

Pro Phe Gly Ala Met Gly Ile Val Ile Thr Gly Asn His Val Ser Ala
20 25 30

Arg Ile Asp Asp Asp His Ile Val Ile Val Ala Pro Arg Pro Glu Ala
35 40 45

Thr Ile Gln Leu Gln Leu Phe Phe Met Pro Gly Gln Arg Pro His Lys
50 55 60

Pro Tyr Ser Gly Thr Val Arg Val Ala Phe Arg Ser Asp Ile Thr Asn
65 70 75 80

Gln Cys Tyr Gln Glu Leu Ser Glu Glu Arg Phe Glu Asn Cys Thr His
85 90 95

Arg Ser Ser Ser Val Phe Val Gly Cys Lys Val Thr Glu Tyr Thr Phe
100 105 110

Ser Ala Ser Asn Arg Leu Thr Gly Pro Pro His Pro Phe Lys Leu Thr
115 120 125

Ile Arg Asn Pro Arg Pro Asn Asp Ser Gly Met Phe Tyr Val Ile Val
130 135 140

Arg Leu Asp Asp Thr Lys Glu Pro Ile Asp Val Phe Ala Ile Gln Leu
145 150 155 160

Ser Val Tyr Gln Phe Ala Asn Thr Ala Ala Thr Arg Gly Leu Tyr Ser
165 170 175

Lys Ala Ser Cys Arg Thr Phe Gly Leu Pro Thr Val Gln Leu Glu Ala
180 185 190

Tyr Leu Arg Thr Glu Glu Ser Trp Arg Asn Trp Gln Ala Tyr Val Ala
195 200 205

Thr Glu Ala Thr Thr Thr Ser Ala Glu Ala Thr Thr Pro Thr Pro Val
210 215 220

Thr Ala Thr Ser Ala Ser Glu Leu Glu Ala Glu His Phe Thr Phe Pro
225 230 235 240

Trp Leu Glu Asn Gly Val Asp His Tyr Glu Pro Thr Pro Ala Asn Glu
245 250 255

Asn Ser Asn Val Thr Val Arg Leu Gly Thr Met Ser Pro Thr Leu Ile
260 265 270

Gly Val Thr Val Ala Ala Val Val Ser Ala Thr Ile Gly Leu Val Ile
275 280 285

Val Ile Ser Ile Val Thr Arg Asn Met Cys Thr Pro His Arg Lys Leu
290 295 300

Asp Thr Val Ser Gln Asp Asp Glu Glu Arg Ser Gln Thr Arg Arg Glu
305 310 315 320

Ser Arg Lys Phe Gly Pro Met Val Ala Cys Glu Ile Asn Lys Gly Ala
325 330 335

Asp Gln Asp Ser Glu Leu Val Glu Leu Val Ala Ile Val Asn Pro Ser
340 345 350

Ala Leu Ser Ser Pro Asp Ser Ile Lys Met .
355 360

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Met	Asn	Met	Leu	Val	Ile	Val	Leu	Ala	Ser	Cys	Leu	Ala	Arg	Leu	Thr
1				5					10					15	
Phe	Ala	Thr	Arg	His	Val	Leu	Phe	Leu	Glu	Gly	Thr	Gln	Ala	Val	Leu
			20					25					30		
Gly	Glu	Asp	Asp	Pro	Arg	Asn	Val	Pro	Glu	Gly	Thr	Val	Ile	Lys	Trp
		35					40					45			
Thr	Lys	Val	Leu	Arg	Asn	Ala	Cys	Lys	Met	Lys	Ala	Ala	Asp	Val	Cys
	50					55					60				
Ser	Ser	Pro	Asn	Tyr	Cys	Phe	His	Asp	Leu	Ile	Tyr	Asp	Gly	Gly	Lys
65					70					75					80
Lys	Asp	Cys	Pro	Pro	Ala	Gly	Pro	Leu	Ser	Ala	Asn	Leu	Val	Ile	Leu
				85					90					95	
Leu	Lys	Arg	Gly	Glu	Ser	Phe	Val	Val	Leu	Gly	Ser	Gly	Leu	His	Asn
			100					105					110		
Ser	Asn	Ile	Thr	Asn	Ile	Met	Trp	Thr	Glu	Tyr	Gly	Gly	Leu	Leu	Phe
		115					120					125			
Asp	Pro	Val	Thr	Arg	Ser	Asp	Glu	Gly	Ile	Tyr	Phe	Arg	Arg	Ile	Ser
	130					135					140				
Gln	Pro	Asp	Leu	Ala	Met	Glu	Thr	Thr	Ser	Tyr	Asn	Val	Ser	Val	Leu
145					150					155					160
Ser	His	Val	Asp	Glu	Lys	Ala	Pro	Ala	Pro	His	Glu	Val	Glu	Ile	Asp
				165					170					175	
Thr	Ile	Lys	Pro	Ser	Glu	Ala	His	Ala	His	Val	Glu	Leu	Gln	Met	Leu
			180					185					190		
Pro	Phe	His	Glu	Leu	Asn	Asp	Asn	Ser	Pro	Thr	Tyr	Val	Thr	Pro	Val
		195				200						205			
Leu	Arg	Val	Phe	Pro	Pro	Thr	Glu	His	Val	Lys	Phe	Asn	Val	Thr	Tyr
		210				215					220				
Ser	Trp	Tyr	Gly	Phe	Asp	Val	Lys	Glu	Glu	Cys	Glu	Glu	Val	Lys	Leu
225					230					235					240
Phe	Glu	Pro	Cys	Val	Tyr	His	Pro	Thr	Asp	Gly	Lys	Cys	Gln	Phe	Pro
				245					250					255	
Ala	Thr	Asn	Gln	Arg	Cys	Leu	Ile	Gly	Ser	Val	Leu	Met	Ala	Glu	Phe
			260					265					270		
Leu	Gly	Ala	Ala	Ser	Leu	Leu	Asp	Cys	Ser	Arg	Asp	Thr	Leu	Glu	Asp
		275					280					285			
Cys	His	Glu	Asn	Arg	Val	Pro	Asn	Leu	Arg	Phe	Asp	Ser	Arg	Leu	Ser
		290				295					300				
Glu	Ser	Arg	Ala	Gly	Leu	Val	Ile	Ser	Pro	Leu	Ile	Ala	Ile	Pro	Lys
305					310					315					320
Val	Leu	Ile	Ile	Val	Val	Ser	Asp	Gly	Asp	Ile	Leu	Gly	Trp	Ser	Tyr
				325					330					335	

Thr Val Leu Gly Lys Arg Asn Ser Pro Arg Val Val Val Glu Thr His
340 345 350

Met Pro Ser Lys Val Pro Met Asn Lys Val Val Ile Gly Ser Pro Gly
355 360 365

Pro Met Asp Glu Thr Gly Asn Tyr Lys Met Tyr Phe Val Val Ala Gly
370 375 380

Val Ala Ala Thr Cys Val Ile Leu Thr Cys Ala Leu Leu Val Gly Lys
385 390 395 400

Lys Lys Cys Pro Ala His Gln Met Gly Thr Phe Ser Lys Thr Glu Pro
405 410 415

Leu Tyr Ala Pro Leu Pro Lys Asn Glu Phe Glu Ala Gly Gly Leu Thr
420 425 430

Asp Asp Glu Glu Val Ile Tyr Asp Glu Val Tyr Glu Pro Leu Phe Arg
435 440 445

Gly Tyr Cys Lys Gln Glu Phe Arg Glu Asp Val Asn Thr Phe Phe Gly
450 455 460

Ala Val Val Glu Gly Glu Arg Ala Leu Asn Phe Lys Ser Ala Ile Ala
465 470 475 480

Ser Met Ala Asp Arg Ile Leu Ala Asn Lys Ser Gly Arg Arg Asn Met
485 490 495

Asp Ser Tyr .

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Met Pro Phe Lys Thr Arg Gly Ala Glu Asp Ala Ala Ala Gly Lys Asn
1 5 10 15

Arg Phe Lys Lys Ser Arg Asn Arg Glu Ile Leu Pro Thr Arg Leu Arg
20 25 30

Gly Thr Gly Lys Lys Thr Ala Gly Leu Ser Asn Tyr Thr Gln Pro Ile
35 40 45

Pro Trp Asn Pro Lys Phe Cys Ser Ala Arg Gly Glu Ser Asp Asn His
50 55 60

Ala Cys Lys Asp Thr Phe Tyr Arg Arg Thr Cys Cys Ala Ser Arg Ser
65 70 75 80

Thr Val Ser Ser Gln Pro Asp Ser Pro His Thr Pro Met Pro Thr Glu
85 90 95

Tyr Gly Arg Val Pro Ser Ala Lys Arg Lys Lys Leu Ser Ser Asp
100 105 110

Cys Glu Gly Ala His Gln Pro Leu Val Ser Cys Lys Leu Pro Asp Ser
115 120 125
Gln Ala Ala Pro Ala Arg Thr Tyr Ser Ser Ala Gln Arg Tyr Thr Val
130 135 140
Asp Glu Val Ser Ser Pro Thr Pro Pro Gly Val Asp Ala Val Ala Asp
145 150 155 160
Leu Glu Thr Arg Ala Glu Leu Pro Gly Ala Thr Thr Glu Gln Thr Glu
165 170 175
Ser Lys Asn Lys Leu Pro Asn Gln Gln Ser Arg Leu Lys Pro Lys Pro
180 185 190
Thr Asn Glu His Val Gly Gly Glu Arg Cys Pro Ser Glu Gly Thr Val
195 200 205
Glu Ala Pro Ser Leu Gly Ile Leu Ser Arg Val Gly Ala Ala Ile Ala
210 215 220
Asn Glu Leu Ala Arg Met Arg Arg Ala Cys Leu Pro Leu Ala Ala Ser
225 230 235 240
Ala Ala Ala Ala Gly Ile Val Ala Trp Ala Ala Ala Arg Ala Leu Gln
245 250 255
Lys Gln Gly Arg
260

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Met Ser Lys Cys Tyr Cys Leu Ala Arg His Leu Tyr Lys Ser Pro Arg
1 5 10 15
Cys Val Gly Arg Arg Val Ala Phe Gly Gly Leu Ala Thr Met Ser Arg
20 25 30
Pro Pro Thr Ser His Leu Asp Leu Ala Phe Ser Ala Ala Phe Arg Gly
35 40 45
Thr Asp Leu Pro Gly Gly Arg Phe Trp Arg Ala Ser Gln Ser Cys Asp
50 55 60
Ile Phe Phe Trp Pro Asp Leu Ala Ala Val Ile Val Gln Ala Ala Arg
65 70 75 80
Ala Tyr Phe Glu Gly Lys Glu Arg Leu Gly Ser Leu Gln Val Ala Glu
85 90 95
Asp Ile Thr Ala His Asp Pro Arg Ile Ala Pro Ala Ala Lys Arg Ala
100 105 110
Val Ala Ala Ala Val Gly Leu Trp Thr Ala Leu Ser Glu Leu Val Gly
115 120 125

Gly Pro Asn Gly Glu Leu Glu Ser Lys Val Trp Gly Lys Gln Ile Pro
130 135 140

Arg Ala Ala Ala Trp Glu Ile Arg Asp Val Pro Lys Val Pro Val Ile
145 150 155 160

Gly Pro Asp Ile Leu Ser Phe Phe Ser Ala Ala Val Glu Leu Pro Val
165 170 175

Leu Tyr Ile Arg Ala Arg Gly Gly Ala His Ser Arg Ser Ala His Trp
180 185 190

Asn Asn Gln Ser Ser Ala Pro Ala Ala Gly Leu Ala Ala Ile Arg Ile
195 200 205

Gly Met Glu Met Val Arg Ser Leu Leu Val Ile Ala Leu Pro Leu Ser
210 215 220

Asn Phe Thr Leu Pro Glu Asp Leu Pro Glu Gly Ser Gln Asn Ser Ile
225 230 235 240

Arg Ala Phe Val Ala His Leu Met Asn Cys Val Ala Thr Asp Lys Ile
245 250 255

Met Ser Pro Asp Val Arg Val Pro Val Glu Glu Ser Phe Tyr Ser His
260 265 270

Cys Leu Arg Glu Ile Ile Met Cys Glu Arg Ala Phe Cys Tyr Pro Cys
275 280 285

Asn Pro Pro Pro Lys Trp .
290

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Met Glu Asn Met Leu Asp Gly Cys Tyr Pro Leu Ala Leu Met Asp Ser
1 5 10 15

Asp His Ile Thr Ala His Ala Val Pro Arg Gly Glu Arg Arg Arg Gln
20 25 30

Gly Ala Ala Val Ala Ser Ser Glu Ser Ala Asp Ser Val Asp Pro Cys
35 40 45

Ile Arg Ile Ala Ser Arg Leu Trp Arg Glu Leu Val Glu Ile Ser Ser
50 55 60

Glu Leu Lys Asp Gly Tyr Gly Glu Phe Thr Ser Ala Arg Asp Arg Arg
65 70 75 80

Asn Ala Leu Ile Ala Ala Asn Glu Arg Leu Arg Ser Ala Phe Leu Gly
85 90 95

Ala Ser Arg Ala Thr Arg Gly Leu Gly Leu Arg Pro Arg Trp Ala Ser
100 105 110

